



; Sequence 36, Application US/09301593A  
; Patent No. 6455677  
; GENERAL INFORMATION:  
; APPLICANT: Park, John E.  
; APPLICANT: Garin-Chesa, Pilar  
; APPLICANT: Bamberger, Uwe  
; APPLICANT: Leger, Olivier  
; APPLICANT: Saldanha, Jose W.  
; APPLICANT: Rettig, Wolfgang J.  
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility  
; CURRENT APPLICATION NUMBER: US/09/301,593A  
; CURRENT FILING DATE: 1999-04-29  
; EARLIER APPLICATION NUMBER: EP 98107925.4  
; EARLIER FILING DATE: 1998-04-30  
; EARLIER APPLICATION NUMBER: US 60/086,049  
; EARLIER FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 36  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-301-593-36

Query Match 91.4%; Score 1136; DB 2; Length 240;  
Best Local Similarity 90.0%; Pred. No. 8.4e-86;  
Matches 216; Conservative 12; Mismatches 12; Indels 0; Gaps 0;  
QY 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNOKNYLA 60  
DB 1 METDTLLWVLLWPGSGDIVMTQSPDSLAVSLGERATINCKSSQSLLYSRNOKNYLA 60  
QY 61 WYQKPGQSPKLLIYWASARESGVDPFRFSGSGGTDFTLTISVQAEADVAVVYCCQYYSY 120  
DB 61 WYQKPGQSPKLLIYWASARESGVDPFRFSGSGGTDFTLTISVQAEADVAVVYCCQYYSY 120  
QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVIVCLNNFPYPRQAKVQWKVDNAL 180  
DB 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVIVCLNNFPYPRQAKVQWKVDNAL 180  
QY 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 240  
DB 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 240

RESULT 3  
US-10-630-406-8  
; Sequence 8, Application US/10630406  
; Patent No. 6887673  
; GENERAL INFORMATION:  
; APPLICANT: Jure-Kunkel, Maria  
; APPLICANT: Ganguly, Subinay  
; APPLICANT: Abraham, Ralph  
; APPLICANT: Hollenbaugh, Diane L.  
; APPLICANT: Rillema, Jill  
; APPLICANT: Thorne, Barbara  
; APPLICANT: Shuford, Walter W.  
; APPLICANT: Mittleer, Robert S.  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN 4-1BB  
; FILE REFERENCE: D0288 NP  
; CURRENT APPLICATION NUMBER: US/10/630,406  
; CURRENT FILING DATE: 2003-07-30  
; PRIOR APPLICATION NUMBER: US 60/399,646  
; PRIOR FILING DATE: 2002-07-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 8  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic

US-10-630-406-8  
Query Match 90.3%; Score 1122; DB 2; Length 240;  
Best Local Similarity 90.0%; Pred. No. 1.2e-84;  
Matches 216; Conservative 10; Mismatches 14; Indels 0; Gaps 0;  
QY 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNOKNYLA 60  
DB 1 MEAPQAQLFLLLWLPDFTGTGDIWMTQSPDSLAVSLGERATINCKSSQSLLYSGNOKNYLA 60  
QY 61 WYQKPGQSPKLLIYWASARESGVDPFRFSGSGGTDFTLTISVQAEADVAVVYCCQYYSY 120  
DB 61 WYQKPGQSPKLLIYWASARESGVDPFRFSGSGGTDFTLTISVQAEADVAVVYCCQYYSY 120  
QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVIVCLNNFPYPRQAKVQWKVDNAL 180  
DB 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVIVCLNNFPYPRQAKVQWKVDNAL 180  
QY 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 240  
DB 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 240

RESULT 4  
US-09-627-896B-22  
; Sequence 22, Application US/09627896B  
; Patent No. 6827934  
; GENERAL INFORMATION:  
; APPLICANT: CO, MAN SUNG  
; APPLICANT: VASQUEZ, MAXIMILIANO  
; APPLICANT: CARENO, BEATRIZ  
; APPLICANT: CELNIKER, ABBIE CHERYL  
; APPLICANT: COLLINS, MARY  
; APPLICANT: GOLDMAN, SAMUEL  
; APPLICANT: GRAY, GARY S.  
; APPLICANT: KNIGHT, ANDREA  
; APPLICANT: O'HARA, DENISE  
; APPLICANT: RUP, BONITA  
; APPLICANT: VELDMAN, GERTRUIDA M.  
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS  
; FILE REFERENCE: 08702.0081-01000  
; CURRENT APPLICATION NUMBER: US/09/627,896B  
; CURRENT FILING DATE: 2000-07-27  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: 3D1 light chain  
US-09-627-896B-22

Query Match 90.2%; Score 1121.5; DB 2; Length 239;  
Best Local Similarity 90.4%; Pred. No. 1.3e-84;  
Matches 217; Conservative 11; Mismatches 11; Indels 1; Gaps 1;  
QY 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNOKNYLA 60  
DB 1 MDSQAQVLMILLWVSGTCGDIWMTQSPDSLAVSLGERATINCKSSQSLLYSRNOKNYLA 60  
QY 61 WYQKPGQSPKLLIYWASARESGVDPFRFSGSGGTDFTLTISVQAEADVAVVYCCQYYSY 120  
DB 61 WYQKPGQSPKLLIYWASARESGVDPFRFSGSGGTDFTLTISVQAEADVAVVYCCQYYSY 120  
QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVIVCLNNFPYPRQAKVQWKVDNAL 180  
DB 121 -YTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVIVCLNNFPYPRQAKVQWKVDNAL 179  
QY 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 240  
DB 180 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 239



; APPLICATION NUMBER: US/08/952,235  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/460368  
; FILING DATE: 02-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P0938P1  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 220 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-08-952-235-1  
  
Query Match 85.6%; Score 1064; DB 2; Length 220;  
Best Local Similarity 90.9%; Pred. No. 6.2e-80;  
Matches 200; Conservative 14; Mismatches 6; Indels 0; Gaps 0;  
  
QY 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNOKNYLAWYQKPGQSPKLLIYWASAR 80  
Db 1 DIMMSQSPSSLTVSVGEKVTVCCKSSQSLTYTSSQKNYLAQQKPGQSPKLLIYWASTR 60  
  
QY 81 ESGVPRDFSGSGGTDFTLTITSSVOAEDVAVYCCQYYGYPLTFAGATKLEKRTVAAPS 140  
Db 61 ESGVPRDFSGSGGTDFTLTITSVKADDLAVYCCQYYAYPWTFGGTTKLEIKRTVAAPS 120  
  
QY 141 VFIFPPSDEQLSGTASVCLLNFPYKAVQKVDNALQSGNSQESVTEQDSKDTYS 200  
Db 121 VFIFPPSDEQLSGTASVCLLNFPYKAVQKVDNALQSGNSQESVTEQDSKDTYS 180  
  
QY 201 LSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
Db 181 LSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
  
RESULT 8  
US-09-669-971-1  
; Sequence 1, Application US/09669971  
; Patent No. 6468529  
; GENERAL INFORMATION:  
; APPLICANT: Schwall, Ralph H.  
; Tabor, Kelly H.  
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor  
; Antagonists and Uses Thereof  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/669,971  
; FILING DATE: 05-JUL-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/952,235  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/460368  
; FILING DATE: 02-JUN-1995  
; ATTORNEY/AGENT INFORMATION:

; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P0938P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 220 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-669-971-1  
  
Query Match 85.6%; Score 1064; DB 2; Length 220;  
Best Local Similarity 90.9%; Pred. No. 6.2e-80;  
Matches 200; Conservative 14; Mismatches 6; Indels 0; Gaps 0;  
  
QY 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNOKNYLAWYQKPGQSPKLLIYWASAR 80  
Db 1 DIMMSQSPSSLTVSVGEKVTVCCKSSQSLTYTSSQKNYLAQQKPGQSPKLLIYWASTR 60  
  
QY 81 ESGVPRDFSGSGGTDFTLTITSSVOAEDVAVYCCQYYGYPLTFAGATKLEKRTVAAPS 140  
Db 61 ESGVPRDFSGSGGTDFTLTITSVKADDLAVYCCQYYAYPWTFGGTTKLEIKRTVAAPS 120  
  
QY 141 VFIFPPSDEQLSGTASVCLLNFPYKAVQKVDNALQSGNSQESVTEQDSKDTYS 200  
Db 121 VFIFPPSDEQLSGTASVCLLNFPYKAVQKVDNALQSGNSQESVTEQDSKDTYS 180  
  
QY 201 LSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
Db 181 LSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
  
RESULT 9  
US-08-812-586-29  
; Sequence 29, Application US/08812586  
; Patent No. 6048704  
; GENERAL INFORMATION:  
; APPLICANT: Martin David Tilson  
; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC  
; PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)  
; TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/812,586  
; FILING DATE: 07-MAR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/53862-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 239 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single



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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-812-586-29

Query Match      82.0%; Score 1019.5; DB 2; Length 239;
Best Local Similarity 85.2%; Pred. No. 3.1e-76; Mismatches 20; Indels 1; Gaps 1;
Matches 201; Conservative 14;

QY 4 QAQVLMALLLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSQNKNYLAWYQ 63
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Db 4 QTQVFISLLLLWISG-AGDIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQ 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 64 QKPGQSPKLLIYWASARESGVDPDRFSGSGSGDTFTLTISVQAEADVAVYYCOQYYSPLT 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 QKPGQAPRLLIYDASSRATGIPDRFSGSGSGDTFTLTISRLEPEDPAVYYGQYGSPLT 122
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 124 FGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQSG 183
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 FGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQSG 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 184 NSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 NSQESVTEQDSKDSYSLSTLTLSKADYKHKVYAGEVTHQGLSSPVTKSFNRGE 238
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-09-535-832A-30
; Sequence 30, Application US/09535832A
; Patent No. 653769
; GENERAL INFORMATION:
; APPLICANT: Tilson, Martin David
; TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
; TITLE OF INVENTION: With Abdominal Aortic Aneurysm (AAA) Disease, and
; TITLE OF INVENTION: Diagnostic and Therapeutic use Thereof
; FILE REFERENCE: 53862-AZ
; CURRENT APPLICATION NUMBER: US/09/535,832A
; CURRENT FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-832A-30

Query Match      82.0%; Score 1019.5; DB 2; Length 239;
Best Local Similarity 85.2%; Pred. No. 3.1e-76; Mismatches 20; Indels 1; Gaps 1;
Matches 201; Conservative 14;

QY 4 QAQVLMALLLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSQNKNYLAWYQ 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 QTQVFISLLLLWISG-AGDIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQ 62
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QY 64 QKPGQSPKLLIYWASARESGVDPDRFSGSGSGDTFTLTISVQAEADVAVYYCOQYYSPLT 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 QKPGQAPRLLIYDASSRATGIPDRFSGSGSGDTFTLTISRLEPEDPAVYYGQYGSPLT 122
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 124 FGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQSG 183
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 FGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQSG 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 184 NSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 NSQESVTEQDSKDSYSLSTLTLSKADYKHKVYAGEVTHQGLSSPVTKSFNRGE 238
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RESULT 11
US-09-472-087-14
; Sequence 14, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.

; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-65

Query Match      80.0%; Score 994.5; DB 2; Length 235;
Best Local Similarity 78.8%; Pred. No. 3.5e-74;
Matches 189; Conservative 27; Mismatches 19; Indels 5; Gaps 1;

QY 1 MDSQAQVLMALLLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSQNKNYLA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 METPAQLLFLLLWLPDITGTEIVLTQSPGTLSLSPGERATLSCRASQSI-----SSSFLA 55
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 WTQOKPGQSPKLLIYWASARESGVDPDRFSGSGSGDTFTLTISVQAEADVAVYYCOQYYSY 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 56 WTQORPGQAPRLLIYDASSRATGIPDRFSGSGSGDTFTLTISRLEPEDPAVYYCOQYGT 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 PUTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNAL 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 116 PWTFGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNAL 175
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 176 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 235
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-09-472-087-65
; Sequence 65, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-65

Query Match      80.0%; Score 994.5; DB 2; Length 235;
Best Local Similarity 78.8%; Pred. No. 3.5e-74;
Matches 189; Conservative 27; Mismatches 19; Indels 5; Gaps 1;

QY 1 MDSQAQVLMALLLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSQNKNYLA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 METPAQLLFLLLWLPDITGTEIVLTQSPGTLSLSPGERATLSCRASQSI-----SSSFLA 55
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDTLTITSSVQAEADVAVVYCOQYYSY 120
Db 56 WYQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCOQYGS 115
QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNAL 180
Db 116 PWTFGGKTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNAL 175
QY 181 QSGNSQESVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 176 QSGNSQESVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 235
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RESULT 13
US-09-472-087-15
; Sequence 15, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-15
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Query Match 79.8%; Score 991.5; DB 2; Length 233;
Best Local Similarity 79.2%; Pred. No. 6e-74;
Matches 190; Conservative 23; Mismatches 20; Indels 7; Gaps 1;

QY 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSQSLIYSGNKNYLA 60
Db 1 METPAQLLFLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSCRTSVS-----SSYLA 53

QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDTLTITSSVQAEADVAVVYCOQYYSY 120
Db 54 WYQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCOQYGS 113

QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNAL 180
Db 114 PTFGGGKTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNAL 173

QY 181 QSGNSQESVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 174 QSGNSQESVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 233
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RESULT 14
US-09-472-087-67
; Sequence 67, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
```

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; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-67
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Query Match 79.8%; Score 991.5; DB 2; Length 233;
Best Local Similarity 79.2%; Pred. No. 6e-74;
Matches 190; Conservative 23; Mismatches 20; Indels 7; Gaps 1;

QY 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSQSLIYSGNKNYLA 60
Db 1 METPAQLLFLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSCRTSVS-----SSYLA 53

QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDTLTITSSVQAEADVAVVYCOQYYSY 120
Db 54 WYQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCOQYGS 113

QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNAL 180
Db 114 PTFGGGKTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNAL 173

QY 181 QSGNSQESVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 174 QSGNSQESVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 233
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RESULT 15
US-09-859-053-34
; Sequence 34, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. 6803039uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-34
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Query Match 79.4%; Score 987; DB 2; Length 236;
Best Local Similarity 78.8%; Pred. No. 1.4e-73;
Matches 190; Conservative 27; Mismatches 18; Indels 6; Gaps 2;

QY 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSQSLIYSGNKNYLA 60
Db 1 METPAQLLFLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSCRAQNI-----RSSYLA 55

QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDTLTITSSVQAEADVAVVYCOQYYSY 120
Db 56 WYQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCOQYGS 115
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QY 5 AQLMLLLLVSGTCDIVMSQSPDSLAVSLGERVTLNCKSSQSLYSQNKNYLAWYQQ 64  
 DB 5 AQLGLLLLVLPGARCAIRMTQSPSFSASTGDRVITCRASQSI-----GSLAWYQQ 58  
 QY 65 KPGQSPKLLIYWASARESVPDRFSGSGSGTDFTLTISVQAEDVAVVYCCQYYSYPLTF 124  
 DB 59 KPGKAPQLLIYAASTLQSGVPRFSGSASGTDFTLTISCLQSDFAFYCCQYTYTPWTF 118  
 QY 125 GAGTKLELKRITVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGN 184  
 DB 119 GGGTKEVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGN 178  
 QY 185 SQESVTEQDSKDYSTLSSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 240  
 DB 179 SQESVTEQDSKDYSTLSSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 234  
 RESULT 12  
 Q6GMX0 HUMAN  
 ID Q6GMX0\_HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6GMX0  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueudin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; BC073775; AAH73775.1; -, mRNA.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR DR  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.

KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;  
 Query Match 77.6%; Score 965; DB 2; Length 236;  
 Best Local Similarity 79.2%; Pred. No. 1.3e-73;  
 Matches 187; Conservative 19; Mismatches 24; Indels 6; Gaps 1;  
 QY 5 AQLMLLLLVSGTCDIVMSQSPDSLAVSLGERVTLNCKSSQSLYSQNKNYLAWYQQ 64  
 DB 7 AQLGLLLLVLPGARCAIRMTQSPSFSASTGDRVITCRASQSI-----NINNYLWYQL 60  
 QY 65 KPGQSPKLLIYWASARESVPDRFSGSGSGTDFTLTISVQAEDVAVVYCCQYYSYPLTF 124  
 DB 61 KPGKAPQLLIYAASLQSGVPRFSGSASGTDFTLTISLQSDFAFYCCQYTYTPWTF 120  
 QY 125 GAGTKLELKRITVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGN 184  
 DB 121 GGGTKEVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGN 180  
 QY 185 SQESVTEQDSKDYSTLSSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 240  
 DB 181 SQESVTEQDSKDYSTLSSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 236  
 RESULT 13  
 Q6GMW1 HUMAN  
 ID Q6GMW1\_HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6GMW1  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE IGKC protein.  
 GN IGKC protein.  
 GN Name=IGKC;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueudin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RG NIH MGC Project;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; BC073791; AAH73791.1; -, mRNA.  
 DR SNR; Q6GMW1; 24-236.  
 DR Ensembl; ENSG00000163245; Homo sapiens.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.

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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 12.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25751 MW; 5BFEGA087AFAC437 CRC64;

Query Match 77.68; Score 965; DB 2; Length 236;
Best Local Similarity 79.7%; Pred. No. 1.3e-73;
Matches 188; Conservative 18; Mismatches 24; Indels 6; Gaps 1;

QY 5 AQLMLLLLVSGTCGDIVMSQSPDSLAIVSLGERVTLNCKSSQSLLYSGNQKNYLAQQ 64
DB 7 AQLGLLLLVLPGARCAIQMTQSPSSLSASVGDRTVITCRASQGI-----SNDLGWYQQ 60

QY 65 KPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFTLTISSVQAEADVAVVYCOQYYSYPLTF 124
DB 61 KPGKAPKLLIYAASSLQSGVPSRFPSGSGSGTDFTLTISSLPQEDFATYYCLQDYNYPWTF 120

QY 125 GAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 184
DB 121 GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 180

QY 185 SQSVTEQDSKDYSTLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
DB 181 SQSVTEQDSKDYSTLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 14
Q723Y4 HUMAN
ID Q723Y4 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q723Y4
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL; BC005332; AH05332.1; -; mRNA.
DR HSPB; P01834; 1HEZ.
DR Ensemble; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KM Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 236 AA; 25702 MW; 7BFEE4ED23084BC6 CRC64;

Query Match 77.5%; Score 963; DB 2; Length 236;
Best Local Similarity 79.7%; Pred. No. 1.9e-73;
Matches 188; Conservative 18; Mismatches 24; Indels 6; Gaps 1;

QY 5 AQLMLLLLVSGTCGDIVMSQSPDSLAIVSLGERVTLNCKSSQSLLYSGNQKNYLAQQ 64
DB 7 AQLGLLLLVLPGARCAIQMTQSPSSLSASVGDRTVITCRASQDI-----SNYLAQQ 60

QY 65 KPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFTLTISSVQAEADVAVVYCOQYYSYPLTF 124
DB 61 KPGKAPKLLIYGASSLQSGVPSRFPSGSGSGTDFTLTISSLPQEDFATYYCOQYKSYPTF 120

QY 125 GAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 184
DB 121 GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 180

QY 185 SQSVTEQDSKDYSTLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
DB 181 SQSVTEQDSKDYSTLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 15
Q502W4 HUMAN
ID Q502W4 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q502W4
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Glandular pool- thyroid;
RC NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC095489; AAH95489.1; -, mRNA.
DR SNR; Q502W4; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig ci.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25936 MW; E2DF79AC18756AA9 CRC64;

Query Match 77.2%; Score 960; DB 2; Length 236;
Best Local Similarity 78.8%; Pred. No. 3.4e-73;
Matches 186; Conservative 20; Mismatches 24; Indels 6; Gaps 1;

Qy 5 AQLMLLLLVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQQ 64
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 7 AQLGLLLLVFPGRVCDIQMTQSPSSLASVGDRTITCRASQGI-----RNDLGWYQQ 60

Qy 65 KPGSPKLLIYWASAREGYDPRFSGSGGTDFTLTISSVQAEADVAYYCCQYYSPLTF 124
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 61 KPGKAPKRLIFAASSLQSGVPSRPSGSGGTFTLTINSIQPEDFATYYCLQYNSYPRTF 120

Qy 125 GAGTKLELKTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGN 184
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 121 GQGTKVEIKKTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGN 180

Qy 185 SQESVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
   |||||||| |||||||| |||||||| |||||||| |||||||| ||||||||
Db 181 SQESVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236
```

Search completed: February 16, 2006, 10:22:55  
Job time : 126.04 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 16, 2006, 10:12:11 ; Search time 134.04 Seconds  
(without alignments)  
1365.094 Million cell updates/sec

Title: US-10-058-069-9

Perfect score: 1243

Sequence: 1 MDSQAQVLMALLLWVGTCG.....EVTHQGLSLSPVTKSFNRGEC 240

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot|05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	998	80.3	240	2	Q6PIH6 HUMAN
2	986	79.3	240	2	Q52164 mus musculus
3	985.5	79.3	235	2	Q6GMV9 HUMAN
4	983.5	79.1	239	2	Q8NEK0 HUMAN
5	983	79.1	236	2	Q6PIL8 HUMAN
6	977.5	78.6	235	2	Q6GMW0 HUMAN
7	977.5	78.6	235	2	Q6PJF2 HUMAN
8	976.5	78.6	239	2	Q8PTCD0 HUMAN
9	975	78.4	236	2	Q6P5S8 HUMAN
10	974	78.4	236	2	Q6GMX8 HUMAN
11	968	77.9	234	2	Q7Z473 HUMAN
12	965	77.6	236	2	Q6GMX0 HUMAN
13	965	77.6	236	2	Q6GMW1 HUMAN
14	963	77.5	236	2	Q7Z3Y4 HUMAN
15	960	77.2	236	2	Q502W4 HUMAN
16	959.5	77.2	239	2	Q6P491 HUMAN
17	958	77.1	236	2	Q6PIT5 HUMAN
18	955	76.8	234	2	Q5EFE6 HUMAN
19	954	76.7	236	2	Q6PIH7 HUMAN
20	953	76.7	236	2	Q6GMX9 HUMAN
21	935	75.2	236	2	Q6PIH4 HUMAN
22	923	74.3	234	2	Q56919 HUMAN
23	809	65.1	241	2	Q632X4 MOUSE
24	804	64.7	238	2	Q58EU4 MOUSE
25	767.5	61.7	239	2	Q58EU8 MOUSE
26	767	61.7	238	2	Q6GJS7 MOUSE
27	752	60.5	234	2	Q4KM66 RAT
28	746.5	60.1	234	2	Q5XKG4 MOUSE
29	746	60.0	234	2	Q5M838 RAT
30	742	59.7	236	2	Q7TS98 MOUSE
31	726	58.4	236	2	Q52L95 MOUSE

#### RESULT 1

ID	Q6PIH6 HUMAN PRELIMINARY;	PRT;	240 AA.
AC	Q6PIH6;		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DE	IGKV1-5 protein.		
GN	Name=IGKV1-5;		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Lung;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603999;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywicki M.I., Skalka U., Smailus D.E.,		
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RL	and mouse cDNA sequences."		
RN	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Lung;		
RC	Director MGC Project;		
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC034142; AAH34142.1; -, mRNA.		
DR	HSSP; P01837; 1KB5.		
DR	SMR; Q6PIH6; 23-240.		
DR	InterPro; IPR003599; Ig.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003597; Ig-cl.		
DR	InterPro; IPR003006; Ig.MHC.		
DR	InterPro; IPR003596; Ig.V.		
DR	Pfam; PF07654; C1-set; 1.		
DR	SMART; SM00409; IG; 2.		
DR	SMART; SM00407; IGcl; 1.		

Q65ZC0 mus musculus  
Q5xfy8 mus musculus  
Q56917 homo sapien  
Q58EV6 mus musculus  
Q569Y8 mus musculus  
Q78236 xenopus lae  
Q6ntus xenopus lae  
Q6ntus xenopus lae  
Q6ntus xenopus lae  
Q5hzc6 xenopus tro  
P06314 homo sapien  
P06313 homo sapien  
P01834 homo sapien  
P06312 homo sapien  
P01625 homo sapien



DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 SQ SEQUENCE 240 AA; 26234 MW; 1804DBBB7815C4 CRC64;  
 Query Match 80.3%; Score 998; DB 2; Length 240;  
 Best Local Similarity 83.1%; Pred. No. 2.1e-76;  
 Matches 197; Conservative 15; Mismatches 23; Indels 2; Gaps 2;  
 QY 5 AQVLMLLWVSGTCGDIWMSQSPDSLAIVSLGERVTLNCKSSQSLYSNGKNYLAQQ 64  
 DB 5 AQLGLMLWVSGSSGDIWVAOSPLSVTPGPAISICRSSLHS-NGNYFDWLIQ 63  
 QY 65 KFGQSPKLIYWASARESGVDPDRFSGSGSGTDFTLTISSVQADVAVYICQ-QYYSPYLT 123  
 DB 64 KFGQSPQLLIYWGSRASGVDPDRFSGSGSGTDFTLKISRVEADVGYYICMQALQPPYT 123  
 QY 124 FGAGTKLEIKRTVAAPSVFIFFPSDEQLSGTASVCLNNFYPREAKVQWKVDNALQSG 183  
 DB 124 FGQGTKEIKRTVAAPSVFIFFPSDEQLSGTASVCLNNFYPREAKVQWKVDNALQSG 183  
 QY 184 NSQESVTEQDSKDYSLSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSNRGC 240  
 DB 184 NSQESVTEQDSKDYSLSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSNRGC 240  
 RESULT 2  
 Q52L64\_MOUSE PRELIMINARY; PRT; 240 AA.  
 AC Q52L64;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Mix FVB/N;  
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zesberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Mix FVB/N;  
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
 RG NIH MGC Project;  
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC094049; AAH94049.1; -; mRNA.  
 DR SNR; Q52L64; 21-240.  
 DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; Igc1; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 240 AA; 26609 MW; CF8630CCCC002B52C CRC64;  
 Query Match 79.3%; Score 986; DB 2; Length 240;  
 Best Local Similarity 76.7%; Pred. No. 2.2e-75;  
 Matches 184; Conservative 25; Mismatches 31; Indels 0; Gaps 0;  
 QY 1 MDSQAVLMLLWVSGTCGDIWMSQSPDSLAIVSLGERVTLNCKSSQSLYSNGKNYLA 60  
 DB 1 MDSQAVLMLLWVSGTCGDIWMSQSPDSLAIVSLGERVTLNCKSSQSLYSNGKNYLA 60  
 QY 61 WYQOKPGQSPKLIYWASARESGVDPDRFSGSGSGTDFTLTISSVQADVAVYICQYYSY 120  
 DB 61 WYQOKPGQSPKLIYWASARESGVDPDRFSGSGSGTDFTLTISSVQADVAVYICQYYSY 120  
 QY 121 PLTFGAGTKLEIKRTVAAPSVFIFFPSDEQLSGTASVCLNNFYPREAKVQWKVDNAL 180  
 DB 121 PLTFGAGTKLEIKRTVAAPSVFIFFPSDEQLSGTASVCLNNFYPREAKVQWKVDNAL 180  
 QY 181 QSGNSQESVTEQDSKDYSLSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSNRGC 240  
 DB 181 RQGVNLNSWTQDSKDYSLSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSNRGC 240  
 RESULT 3  
 Q6GMV9\_HUMAN PRELIMINARY; PRT; 235 AA.  
 AC Q6GMV9;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zesberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.



```
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073793; AAH73793.1; -; mRNA.
DR SNR; O6GNV9; 21-235;
DR GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;

Query Match 79.3%; Score 985.5; DB 2; Length 235;
Best Local Similarity 78.8%; Pred. No. 2.3e-75;
Matches 189; Conservative 27; Mismatches 19; Indels 5; Gaps 2;

QY 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERTVLTNCKSSQSLYSNGNQNYLA 60
DB 1 METPAQLLFLLMLPDIITGEIVLTQSPGTLISLSPGERAALSCRAQSV----NSK-YLA 55

QY 61 WYQKQSQPKLIYASARESVPDRFSGSGGTDTFTLTISVQAEADVAVYCOQYYS 120
DB 56 WYQKQSQPKLIYASARESVPDRFSGSGGTDTFTLTISVQAEADVAVYCOQYYS 115

QY 121 PLTFGAGTGLKLRKTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNAL 180
DB 116 PLTFGGGTRVKIKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNAL 175

QY 181 QSGNSQESVTEQDSKOSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 240
DB 176 QSGNSQESVTEQDSKOSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 235

RESULT 4
Q8NEKO HUMAN
ID Q8NEKO HUMAN PRELIMINARY; PRT; 239 AA.
AC Q8NEKO;
DT 01-OCT-2002 (T:EMBLrel. 22, Created)
DT 01-OCT-2002 (T:EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T:EMBLrel. 26, Last annotation update)
DE IGKV1-5 protein.
GN Name=IGKV1-5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.J., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RA Director MGC Project;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed-1601042;
RA Huber C., Klobeck H.G., Zachau H.G.;
RT "Ongoing V kappa-J kappa recombination after formation of a productive
V kappa-J kappa coding joint.";
RL Eur. J. Immunol. 22:1561-1565(1992).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed-8258341;
RA Wagner S.D., Luzzatto L.;
RT "v kappa gene segments rearranged in chronic lymphocytic leukemia are
distributed over a large portion of the V kappa locus and do not show
somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX PubMed-8258341;
RA Klein R., Jaenichen R., Zachau H.G.;
RT "Expressed human immunoglobulin kappa genes and their hypermutation.";
RL Eur. J. Immunol. 23:3248-3262(1993).
DR EMBL; BC030814; AAH30814.1; -; mRNA.
DR PIR; S23638; S23638.
DR PIR; S34091; S34091.
DR PIR; S40342; S40342.
DR PIR; S40357; S40357.
DR HSSP; P01834; 1172.
DR SMR; Q8NEKO; 21-237.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 79.1%; Score 983.5; DB 2; Length 239;
Best Local Similarity 81.8%; Pred. No. 3.5e-75;
Matches 193; Conservative 15; Mismatches 27; Indels 1; Gaps 1;

QY 5 AQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERTVLTNCKSSQSLYSNGNQNYLA 64
DB 5 AQVLMILLWVSGSGSDIVMTQSPSLPTPGEPASISCRSSQSLHSDGY-NYLDWYLQ 63

QY 65 KQGSPKLIYASARESVPDRFSGSGGTDTFTLTISVQAEADVAVYCOQYYSPLTF 124
DB 64 KPGQSPQLIYLGSRNAGVPDRFSGSGGTDTFTLTISKVEADVGIYVCMQGLQTPQTF 123

QY 125 GAGTKLELRKTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNAL 184
DB 124 GQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNTLQSGN 183

QY 185 QGSVTEQDSKOSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 240
DB 184 SQESVTEQDSKOSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 5
Q6PIL8_HUMAN
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[illegible]

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Db 1 MEAPAQLLFLLWLLPDSGTGEIWMVQSPATLSVSPGERATLSGRASQSI-----SNLTA 54
QY 61 WYQKQPSQKLIYASARESGVDPDRFSGSGSGTDFTLTISVQAEADVAVYVCOQYYS 120
Db 55 WYQORFQAPRLLIYAGSSRVGTGIPGRFSGSGSGTDFTLTISVQAEADVAVYVCOQYNDW 114
QY 121 PL-TFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNA 179
Db 115 LLATFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNA 174
QY 180 LOSGNSQESVTEQDSKDYSLSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGE 239
Db 175 LOSGNSQESVTEQDSKDYSLSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGE 234
QY 240 C 240
Db 235 C 235

RESULT 7
Q6PJF2 HUMAN
ID Q6PJF2 HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6PJF2; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016380; AAH16380.1; -; mRNA.
DR HSP; P01837; IKCU.
DR SNR; O6PJF2; 21-235.
DR InterPro; IPR003593; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG1; 2.
DR SMART; SM00407; IG1; 1.
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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match 78.6%; Score 977.5; DB 2; Length 235;
Best Local Similarity 77.9%; Pred. No. 1.1e-74;
Matches 187; Conservative 27; Mismatches 21; Indels 5; Gaps 1;

QY 1 MDSQAOVLMLLLWVSGTGDIVMSQSPDSLAVSLGRVTLNCKSSQSLLYSGNKNVLA 60
Db 1 METPAGFLFLLWLPQTGTEI VLTQSPATLSVSPGERATLSRASQIV-----SSAYLA 55
QY 61 WYQKQPSQKLIYASARESGVDPDRFSGSGSGTDFTLTISVQAEADVAVYVCOQYYS 120
Db 56 WYQKQPSQKLIYASARESGVDPDRFSGSGSGTDFTLTISVQAEADVAVYVCOQYYS 115
QY 121 PL-TFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNA 180
Db 116 QGTFGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNA 175
QY 181 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 240
Db 176 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 235

RESULT 8
Q8TCD0 HUMAN
ID Q8TCD0 HUMAN PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1598223;
RA Hirabayashi Y., Munakata Y., Sasaki T., Sano H.;
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RT "Variable regions of a human anti-DNA antibody O-81 possessing lupus  
 RT nephritis-associated idiotype.";   
 RL Nucleic Acids Res. 20:2601-0(1992).   
 RP [4]   
 RN NUCLEOTIDE SEQUENCE.   
 RX PubMed=1551402;   
 RA Lautner-Rieske A., Huber C., Meindl A., Pargent W., Schable K.F.,   
 RA Thiele R., Zocher I., Zachau H.G.;   
 RT "The human immunoglobulin kappa locus. Characterization of the   
 RT duplicated A regions.";   
 RL Eur. J. Immunol. 22:1023-1029(1992).   
 RN [5]   
 RP NUCLEOTIDE SEQUENCE.   
 RX PubMed=8258341;   
 RA Klein R., Jaenichen R., Zachau H.G.;   
 RT "Expressed human immunoglobulin kappa genes and their hypermutation.";   
 RL Eur. J. Immunol. 23:3248-3262(1993).   
 RN [6]   
 RP NUCLEOTIDE SEQUENCE.   
 RX PubMed=8436174;   
 RA Wagner S.D., Luzzatto L.;   
 RT "v kappa gene segments rearranged in chronic lymphocytic leukemia are   
 RT distributed over a large portion of the V kappa locus and do not show   
 RT somatic mutation.";   
 RL Eur. J. Immunol. 23:391-397(1993).   
 DR EMBL; BC022362; AAH22362.1; -; mRNA.   
 DR PIR; S22658; S22658.   
 DR PIR; S34095; S34095.   
 DR PIR; S40324; S40324.   
 DR PIR; S40374; S40374.   
 DR PIR; S42267; S42267.   
 DR PIR; S42268; S42268.   
 DR HSSP; P01834; 1172.   
 DR SMR; Q87CD0; 21-237.   
 DR InterPro; IPR007110; Ig-like.   
 DR InterPro; IPR003597; Ig cl.   
 DR InterPro; IPR003006; Ig\_MHC.   
 DR InterPro; IPR003596; Ig\_v.   
 DR Pfam; PF07654; C1-set; 1.   
 DR SMART; SM00406; IGV; 1.   
 DR PROSITE; PS00835; IG\_LIKE; 2.   
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.   
 KW Hypothetical protein; Immunoglobulin domain.   
 SQ SEQUENCE 239 AA; 26235 MW; FAGEDCA3B03871D CRC64;   
 Query Match 78.6%; Score 976.5; DB 2; Length 239;   
 Best Local Similarity 80.2%; Pred. No. 1.4e-74;   
 Matches 190; Conservative 22; Mismatches 22; Indels 3; Gaps 2;   
 QY 5 AQLMLLLVWVGTCGDIIVMSQSPDSLAVSLGERTVLNCKSSQSLIYS-GNKNYLAWYQ 63  
 DB 5 AQLGLLLWVPGSSGDVMTQPSLSLPTVLGQPASISCRSTQSLVYSDGN--TYLWFPQ 62  
 QY 64 QKPGQSPKLLIYWASARESGVPRFSGSGGTDTFTLTISVQAEADVAVYVCOQYSPILT 123  
 DB 63 QRPGQSPRLIYKVNRSRSGVPRFSGSGGTDTFTLTITRVEADVGVYFCMOGTHWPT 122  
 QY 124 FGAGTKLELKRITVAAPSVFIFFPSDEQLKSGTASVCLLNFPYREAKVQWKVDNALQSG 183  
 DB 123 FGGTKLEIKRTVAAPSVFIFFPSDEQLKSGTASVCLLNFPYREAKVQWKVDNALQSG 182  
 QY 184 NSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
 DB 183 NSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
 RESULT 9  
 Q6P558 HUMAN  
 ID Q6P558 HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6P558;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.   
 OS Homo sapiens (Human).   
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;   
 OC Homo.   
 NCBI\_TaxID=9606;   
 RN [1]   
 RP NUCLEOTIDE SEQUENCE.   
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;   
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,   
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,   
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,   
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,   
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,   
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,   
 RA Brownstein M.J., Ustin T.B., Toehiyuki S., Carninci P., Prange C.,   
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,   
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,   
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,   
 RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,   
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,   
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,   
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,   
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,   
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,   
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;   
 RT "Generation and initial analysis of more than 15,000 full-length human   
 RT and mouse cDNA sequences.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).   
 RN [2]   
 RP NUCLEOTIDE SEQUENCE.   
 RX TISSUE=Glandular pool- thyroid;   
 RA Strausberg R.;   
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.   
 DR EMBL; BC062704; AAH62704.1; -; mRNA.   
 DR HSSP; P01837; 1KCU.   
 DR SMR; Q6P558; 21-236.   
 DR InterPro; IPR003599; Ig.   
 DR InterPro; IPR007110; Ig-like.   
 DR InterPro; IPR003597; Ig cl.   
 DR InterPro; IPR003006; Ig\_MHC.   
 DR InterPro; IPR003596; Ig\_v.   
 DR Pfam; PF07654; C1-set; 1.   
 DR SMART; SM00409; IG; 2.   
 DR SMART; SM00407; IGV; 1.   
 DR SMART; SM00406; IGV; 1.   
 DR PROSITE; PS00835; IG\_LIKE; 2.   
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.   
 KW Hypothetical protein.   
 SQ SEQUENCE 236 AA; 25773 MW; 953B37BEB4FF5F27 CRC64;   
 Query Match 78.4%; Score 975; DB 2; Length 236;   
 Best Local Similarity 77.6%; Pred. No. 1.8e-74;   
 Matches 187; Conservative 29; Mismatches 19; Indels 6; Gaps 2;   
 QY 1 MDSQAQVLMMLLLVWVGTCGDIIVMSQSPDSLAVSLGERTVLNCKSSQSLIYS-GNKNYLA 60  
 DB 1 METPAQLLLFLLMLPDTTGEIVLTQSPGTLSPFSGERATLSCRASQTFFSS-----HLA 55  
 QY 61 WYQKQSPKLLIYWASARESGVPRFSGSGGTDTFTLTISVQAEADVAVYVCOQYYSY 120  
 DB 56 WYQQRPGAPRLIYGAASRATGIPRFGSGSGGTDTFTLTITRLEDFAVYFCQYGTGS 115  
 QY 121 P-LTFGAGTKLELKRITVAAPSVFIFFPSDEQLKSGTASVCLLNFPYREAKVQWKVDNA 179  
 DB 116 PSLTFGGTFEIKRTVAAPSVFIFFPSDEQLKSGTASVCLLNFPYREAKVQWKVDNA 175  
 QY 180 LOSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 239  
 DB 176 LOSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 235  
 QY 240 C 240

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 16, 2006, 10:18:02 ; Search time 20.202 Seconds  
(without alignments)  
1143.055 Million cell updates/sec

Title: US-10-058-069-9  
Perfect score: 1243  
Sequence: 1 MDSQAOVLMILLWVSGTCG.....EVTHQGLSSPVTKSFNRGEC 240  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	975	78.4	240	2 S06084	Ig kappa chain pre
2	972	78.2	216	2 JE0241	Ig kappa chain Am3
3	936.5	75.3	215	2 JE0242	Ig kappa chain NIG
4	926.5	74.5	215	2 JE0244	Ig kappa chain NIG
5	894.5	72.0	215	2 A23746	Ig kappa chain V-I
6	887.5	71.4	215	2 JE0243	Ig kappa chain NIG
7	833	67.0	220	2 A31790	Ig kappa chain V r
8	800	64.4	214	2 S68212	Ig kappa chain (Ma
9	757.5	60.9	225	2 S37484	Ig kappa chain - m
10	737	59.3	234	2 S14237	Ig kappa chain pre
11	728.5	58.6	219	2 S38865	Ig kappa chain - m
12	727.5	58.5	219	2 S52028	Ig kappa chain - m
13	727.5	58.5	230	2 S33161	Ig kappa chain - s
14	725.5	58.4	217	2 S42772	Ig kappa chain - m
15	724.5	58.3	219	2 PC4203	Ig kappa chain (mo
16	722	58.2	218	2 S68241	Ig kappa chain V r
17	722	58.1	218	2 JC5810	monoclonal antibod
18	718.5	57.8	219	2 S16112	Ig kappa chain V r
19	718	57.8	234	2 S01320	Ig kappa chain pre
20	700.5	56.4	235	2 S25058	Ig kappa chain - m
21	696.5	56.0	225	2 JL0029	Ig kappa chain pre
22	675	54.3	210	2 A56169	Ig kappa chain V r
23	662	53.3	145	2 PL0014	Ig kappa chain pre
24	633	50.9	178	2 PT0219	Ig kappa chain V-C
25	619	49.8	138	2 S26040	Ig kappa chain pre
26	614	49.4	134	2 PC1214	Ig kappa chain pre
27	613.5	49.4	197	2 S29593	Ig kappa chain (WM
28	595	47.9	135	2 S52059	JC-kappa protein -
29	595.5	47.1	238	2 A49633	Ig lambda-like cha

ALIGNMENTS

RESULT 1

S06084  
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C;Species: Rattus norvegicus (Norway rat)  
C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000  
C;Accession: S06084  
R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.  
Nucleic Acids Res. 17, 7992, 1989  
A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDN  
A;Reference number: S06084; MUID:90016888; PMID:2508067  
A;Accession: S06084  
A;Molecule type: mRNA  
A;Residues: 1-240 <CRO>  
A;Cross-references: UNIPARC:UPI0000113764; EMBL:X16129; NID:q56457; PIDN:CAA34256.1; PI  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-240/Product: Ig kappa chain #status predicted <MAT>  
F;153-222/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 975; DB 2; Length 240;

Best Local Similarity 76.2%; Pred. No. 4.2e-60;

Matches 183; Conservative 20; Mismatches 37; Indels 0; Gaps 0;

Qy	1	MDSQAQVLMILLWVSGTCGDIWMSQSPDSLAVSLAGERVTLNCKSSQSLYSQGNQNYLA	60
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Qy	121	PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQVKNAL	180
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Qy	181	QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYERHKVYACEVTHQGLSSPVTKSFNRGEC	240
Db	181	RRDGVLDVTDQDSKDSTYSMSSTLSLSKADYESHNLTYCEVHVKTSSTSPVWKSFNNEC	240

RESULT 2

JE0241  
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C;Species: Homo sapiens (man)  
C;Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C;Accession: JE0241  
R;Allim, M.A.; Yanaki, S.; Hosain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda,  
submitted to JIPID, November 1998  
A;Description: Structure relationship of kappa type light chains with AL amyloidosis: Mu  
A;Reference number: JE0241  
A;Accession: JE0241











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Db 1 QLLGLLLWLLPGARCDIQVTQSPSSLSASLTERVSITCRTSQSV-----SNVLNMYQQ 54  
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Db 55 KPGQAPKLLIYYATRLTDVPSRFSGSGSGTDYTLTISNLEANDATYYICLOVESTPLAF 114  
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Db 175 FQNSFTDQDQSKSTYSLSSTLTLSSEYQSHNAVACEVSHKSLPTALVKVSNKNEC 230  
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S42772  
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C:Species: Mus musculus (house mouse)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S42772  
R:Schellekens, G.A.  
submitted to the EMBL Data Library, November 1993  
A:Reference number: S42771  
A:Accession: S42772  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-217 <SCH>  
A:Cross-references: UNIPARC:UPI00001161CD; EMBL:X75536; NID:g414143; PIDN:CAA53226.1; PT  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:14-93/Domain: immunoglobulin homology <IMH>  
Query Match 58.4%; Score 725.5; DB 2; Length 217;  
Best Local Similarity 63.3%; Pred. No. 5.1e-43;  
Matches 138; Conservative 31; Mismatches 48; Indels 1; Gaps 1;  
Qy 23 VMSQSPDSLAVSLGERVTLNCKSSQSLYSQKKNYLAWYQKPGQSPKLLIYWASARES 82  
Db 1 VMTQSPSLPVSIGDQASISCRSSQSLVHT-NGNTYLHWYLQKPGQSPKLLIYKVSTRFS 59  
Qy 83 GVPDRFSGSGSGTDFTLTISVQAEDVAVYYCOQYYSYPLTFGAGTKLELKRVAAPSVF 142  
Db 60 GVPDRFSGSGSGTDFTFKISRVEAEDLGIVFCQSSTVVPFTFGSGTKLEIKRADAPTVS 119  
Qy 143 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQVMDNALQSGNSQESVTEQDQSKDSTYSL 202  
Db 120 IFPPSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQGVNLNSWTDQDQSKDSTYMS 179  
Qy 203 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
Db 180 STLTLDKDEYERHNSYTCETHTKTSTSPIVKSFNRGEC 217  
RESULT 15  
PC4203  
Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Dec-1996 #sequence\_revision 31-Dec-1996 #text\_change 11-Jan-2000  
C:Accession: PC4203  
R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.  
Gene 173, 257-259, 1996  
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a m  
A:Reference number: PC4202; MUID:97082978; PMID:8964510  
A:Accession: PC4203  
A:Molecule type: mRNA  
A:Residues: 1-219 <KWA>  
A:Cross-references: UNIPARC:UPI00001157E4; GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID  
C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:1-112/Domain: V region #status predicted <VRG>  
F:113-219/Domain: C region #status predicted <CRG>

Query Match 58.3%; Score 724.5; DB 2; Length 219;  
Best Local Similarity 62.7%; Pred. No. 6e-43;  
Matches 138; Conservative 32; Mismatches 49; Indels 1; Gaps 1;  
Qy 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLYSQKKNYLAWYQKPGQSPKLLIYWASAR 80  
Db 1 DVLMTQTPLSLPVSIGDQASISCRSSQSI VHT-NGNTYLEWYLQKPGQSPKLLIYKVSNR 59  
Qy 81 ESGVPRDFSGSGSGTDFTLTISVQAEDVAVYYCOQYYSYPLTFGAGTKLELKRVAAPS 140  
Db 60 FSGVPRDFSGSGSGTDFTLKISRVEAEDLGIVYCFQGSHPVPTFGGGTKLEIKRADAPT 119  
Qy 141 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQVMDNALQSGNSQESVTEQDQSKDSTYS 200  
Db 120 VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQGVNLNSWTDQDQSKDSTYS 179  
Qy 201 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
Db 180 MSSTLTLTLDKDEYERHNSYTCETHTKTSTSPIVKSFNRNEC 219

Search completed: February 16, 2006, 10:23:49  
Job time : 21.202 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February '16, 2006, 10:12:02 ; Search time 132.121 Seconds  
(without alignments)  
798.138 Million cell updates/sec

Title: US-10-058-069-9  
Perfect score: 1243  
Sequence: 1 MDSQAVMLLLVWSGTGCG.....EVTHQGLSPVTKSFRNGEC 240

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing, first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1243	100.0	240	AAE27927	Aae27927 Human CC4
2	1243	100.0	240	AB882836	Abb82836 Antibody
3	1166	93.8	240	AAY50156	Aay50156 Chimeric
4	1140	91.7	220	ADW77046	Adw77046 Light cha
5	1140	91.7	220	ADW44589	Adw44589 Antibody
6	1136	91.4	240	AAY50161	Aay50161 Human res
7	1135	91.3	220	ADW77054	Adw77054 Light cha
8	1132	91.1	240	ADW23408	Adw23408 Human L61
9	1132	91.1	240	ADZ51047	Adz51047 Amino aci
10	1132	91.1	240	ADZ56181	Adz56181 Protein s
11	1127.5	90.7	241	ADW23426	Adw23426 Human L55
12	1125.5	90.5	239	ADV92470	Adv92470 SW5-1 chl
13	1125.5	90.5	239	ADV98533	Adv98533 Novel chl
14	1125	90.5	240	AAU00815	Aau00815 Human Imm
15	1122	90.3	240	ADJ65029	Adj65029 Plasmid p
16	1120.5	90.1	241	AAE28809	Aae28809 Vector pM
17	1119.5	90.1	241	AE845897	Aeb45897 Human mon
18	1115	89.7	240	AEA41033	Aea41033 Human mon
19	1105.5	88.9	241	AE845859	Aeb45859 Human mon
20	1090	87.7	244	AAV96305	Aay96305 Human IGF
21	1082	87.0	220	ADK52314	Adk52314 Human ant
22	1072.5	86.3	238	ADL23055	Adl23055 Humanised
23	1072.5	86.3	238	ADS88804	Ads88804 Humanised
24	1070	86.1	220	AAY50172	Aay50172 Antibody

ALIGNMENTS

RESULT 1  
AAE27927  
ID AAE27927 standard; protein; 240 AA.  
XX  
AC AAE27927;  
XX  
DT 27-DEC-2002 (first entry)  
XX  
DE Human CC49 antibody light chain protein.  
XX  
KW Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;  
KW neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;  
KW non-Hodgkin's lymphoma; haematologic malignancy; tumour.  
XX  
OS Homo sapiens.  
XX  
PN WO200260955-A2.  
XX  
PD 08-AUG-2002.  
XX  
PF 29-JAN-2002; 2002WO-US002373.  
XX  
PR 29-JAN-2001; 2001US-0264318P.  
PR 16-NOV-2001; 2001US-0331481P.  
(IDEC-) IDEC PHARM CORP.  
PI Braslawsky GR, Hanna N, Chinn P;  
DR WPI; 2002-698547/75.  
DR N-PSDB; AAD45756.  
PT Novel domain deleted CC49 antibody reactive with tumor associated antigen  
PT -72, or C2B8 antibody reactive with CD20, useful for treating  
PT myelosuppressed patient suffering from a neoplastic disorder.  
Example 1; Fig 5A; 74pp; English.  
CC The present invention relates to domain deleted CC49 or C2B8 antibodies.  
CC Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain  
CC deleted sequence in which CH2 domain has been deleted and are reactive  
CC with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive  
CC with CD20 and comprise a heavy chain having a sequence of a derived  
CC domain deleted C2B8 construct where the CH2 domain has been deleted.  
CC Sequences of the invention are useful for imaging a neoplasm. They are  
CC also useful for treating myelosuppressed patients suffering from  
CC neoplastic disorder such as haematologic neoplasm, preferably non-

CC Hodgkin's lymphoma. Antibodies of the invention are also used to treat  
CC neoplastic disorder, colon cancer and haematologic malignancy. They are  
CC useful for reducing tumour size, inhibiting tumour growth and/or  
CC prolonging the survival time of tumour-bearing animals and for treating  
CC tumours. The present sequence is human CC49 light chain protein. This  
CC sequence is used in the exemplification of the invention  
XX  
SQ Sequence 240 AA;  
Query Match 100.0%; Score 1243; DB 5; Length 240;  
Best Local Similarity 100.0%; Pred. No. 4.3e-67;  
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDSQAQVLMALLLWVSGTCGDI VMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKQNYLA 60  
Db 1 MDSQAQVLMALLLWVSGTCGDI VMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKQNYLA 60  
QY 61 WYQQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDFLTITSSVQAEDVAVYCCQYYSY 120  
Db 61 WYQQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDFLTITSSVQAEDVAVYCCQYYSY 120  
QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180  
Db 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180  
QY 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKEHKVYACEVTHOGLSSPVTKSFNRGEC 240  
Db 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKEHKVYACEVTHOGLSSPVTKSFNRGEC 240  
RESULT 2  
AB82836  
ID ABB82836 standard; protein; 240 AA.  
XX ABB82836;  
AC  
XX 31-MAR-2003 (first entry)  
XX  
DE Antibody huCC49 light chain.  
XX  
DE  
KW CC49; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;  
KW vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;  
KW thymometric; hepatotropic; haemostatic; antileprotic; antibacterial;  
KW neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer;  
KW dermatological; immunosuppressive; antiinflammatory.  
XX  
OS Homo sapiens.  
XX  
XX WO200296948-A2.  
XX  
XX 05-DEC-2002.  
XX  
XX 29-JAN-2002; 2002WO-US002374.  
XX  
XX 29-JAN-2001; 2001US-0264318P.  
XX  
XX 16-NOV-2001; 2001US-0331481P.  
XX  
XX 21-DEC-2001; 2001US-0341858P.  
XX  
XX (IDEC-) IDEC PHARM CORP.  
XX  
XX Braislaweky GR, Hanna N, Chinn P, Hariharan K;  
XX  
XX WPI; 2003-140446/13.  
XX  
XX N-PSDB; AB224020.  
XX  
XX Novel dimeric antibody useful for treating immune disorder and neoplastic  
XX disorder, has several non-covalently associated monomeric subunits.  
XX  
XX Example 1; Fig 5A; 78pp; English.  
XX  
XX The invention relates to a dimeric antibody (I) comprising several  
XX monomeric subunits, where the monomeric subunits are non-covalently  
XX associated. (I) is useful for treating a disorder, especially immune  
XX

CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,  
CC resistant Hodgkin's disease high grade, low grade and intermediate grade  
CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),  
CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular  
CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,  
CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic  
CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,  
CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,  
CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small  
CC cleaved and large cell lymphomas, in a mammal (see AB224017 for a  
CC detailed description of the various uses of (I)). The present sequence  
XX represents the antibody huCC49 light chain  
SQ Sequence 240 AA;  
Query Match 100.0%; Score 1243; DB 6; Length 240;  
Best Local Similarity 100.0%; Pred. No. 4.3e-67;  
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDSQAQVLMALLLWVSGTCGDI VMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKQNYLA 60  
Db 1 MDSQAQVLMALLLWVSGTCGDI VMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKQNYLA 60  
QY 61 WYQQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDFLTITSSVQAEDVAVYCCQYYSY 120  
Db 61 WYQQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDFLTITSSVQAEDVAVYCCQYYSY 120  
QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180  
Db 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180  
QY 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKEHKVYACEVTHOGLSSPVTKSFNRGEC 240  
Db 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKEHKVYACEVTHOGLSSPVTKSFNRGEC 240  
RESULT 3  
AAY50156  
ID AAY50156 standard; protein; 240 AA.  
XX AAY50156;  
XX  
XX 17-OCT-2003 (revised)  
DT 31-JAN-2000 (first entry)  
XX  
XX Chimeric mouse/human F19 antibody light chain.  
XX  
XX Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;  
KW humanisation; complementarity determining region; CDR; CDR grafting;  
KW reactive stroma; fibroblast; epithelial cancer; diagnosis;  
KW immune response; framework sequence; constant region; variable region;  
KW producibility; treatment; cancer; colorectal; lung; breast; head; neck;  
KW ovarian; lung; bladder; pancreatic; metastasis; detection; wound healing;  
KW skin inflammation; tumour; immunogenicity; chimeric; light chain.  
XX  
XX Mus sp.  
XX  
XX Homo sapiens.  
XX Chimeric.  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..20 /note= "Leader peptide"  
XX Protein 21..240 /note= "Mature chimeric mouse/human F19 light chain"  
XX Region 21..140 /note= "Mature mouse F19 light chain variable region"  
XX Region 44..60 /note= "CDR 1"  
XX Region 76..82 /note= "CDR 2"  
XX Region 115..123 /note= "CDR 3"  
XX Region 141..240



```
XX SQ Sequence 220 AA;
Query Match 91.7%; Score 1140; DB 9; Length 220;
Best Local Similarity 100.0%; Pred. No. 6.1e-61;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKYNLAWYQKPGQSPKLLIYWASAR 80
DB 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKYNLAWYQKPGQSPKLLIYWASAR 60
QY 81 ESGVDPDRFSGSGGTDFTLTISVVQAEADVAVVYCOQYYSYPLTFGAGTKLEKRTVAAPS 140
DB 61 ESGVDPDRFSGSGGTDFTLTISVVQAEADVAVVYCOQYYSYPLTFGAGTKLEKRTVAAPS 120
QY 141 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 200
DB 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180
QY 201 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 240
DB 181 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 5
ADW44589
ID ADW44589 standard; protein; 220 AA.
XX AC ADW44589;
XX DT 24-MAR-2005 (first entry)
XX DE Antibody huCC49 light chain (CH2 domain deleted).
KW Antibody engineering; bispecific antibody; Cytostatic; Immunosuppressive;
KW Antiinflammatory; Gastrointestinal-Gen.; Dermatological; Antiulcer;
KW Antirheumatic; Antiarthritic; Nephrotropic; Antithyroid; Thyromimetic;
KW Muscular-Gen.; Neuroprotective; Antianemic; CNS-Gen.; Respiratory-Gen.;
KW Vulnerary; cancer; neoplasm; lymphoma; autoimmune disease; inflammation;
KW huCC49; Tag72; light chain variable region.
XX OS Mus sp.
XX OS Homo sapiens.
XX OS Synthetic.
XX OS Chimeric.
XX PN WO2005000899-A2.
XX PD 06-JAN-2005.
XX PF 28-JUN-2004; 2004WO-US020945.
XX PR 27-JUN-2003; 2003US-0483877P.
XX PR 03-OCT-2003; 2003US-0508810P.
XX PR 28-OCT-2003; 2003US-0515311P.
XX PR 30-OCT-2003; 2003US-0516030P.
XX PA (BIOG-) BIOGEN IDEC MA INC.
XX GL Glaser S, Reff M, Yang T, Wu X, Chinn P;
XX WPI; 2005-058133/06.
XX N-PSDB; ADW44586.
XX New composition comprising polypeptide dimers comprising at least four
XX binding sites and at least two polypeptide chains linked via at least one
XX interchain disulfide linkage, useful for treating e.g., cancer or
XX autoimmune diseases.
XX Claim 35; SEQ ID NO 21; 172pp; English.
XX The invention relates to a composition comprising polypeptide dimers
XX comprising at least four binding sites and at least two polypeptide
```

```
CC chains, where the polypeptide chains comprise at least one heavy chain
CC portion and a synthetic connecting peptide, and where greater than about
CC 50% of the dimers comprise polypeptide chains that are linked via at
CC least one interchain disulfide linkage, or comprising minibody molecules
CC comprising two polypeptide chains, where the polypeptide chains comprise
CC a heavy chain portion and a synthetic connecting peptide, where the
CC polypeptide chains lack all or part of a CH2 domain, and where greater
CC than about 50% of the molecules are present in a form in which one of the
CC polypeptide chains are linked via at least one interchain disulfide
CC linkage. Also included are a nucleic acid molecule comprising a
CC nucleotide sequence encoding a polypeptide chain as defined above, a host
CC cell comprising a vector and a binding molecule comprising CH2 deleted
CC heavy and light chains of the antibodies huCC49 and PRIMATIZED p3E8. The
CC synthetic connecting peptide comprises a (Gly-Ser)n linker attached to a
CC portion of a hinge region from IgG1, IgG3 or IgG4. The molecules are
CC bispecific and comprise at least one binding site specific for a soluble
CC ligand or for a cell surface molecule. The molecules comprise two binding
CC sites specific for a tumor cell antigen and two binding sites specific
CC for a prodrug. The synthetic connecting peptide comprises a proline
CC residue at position 243. Kabat numbering system. The synthetic connecting
CC peptide further comprises an alanine residue at position 244 and a
CC proline residue at position 245, Kabat numbering system. The polypeptide
CC dimers are tetraivalent minibody molecules. The composition is useful for
CC treating a subject that would benefit from treatment with an antigen
CC binding molecule, where the subject is suffering from cancer, lymphoma,
CC an autoimmune disease or disorder, or an inflammatory disease or disorder
CC The composition is useful for treating autoimmune diseases such as
CC Crohn's disease, inflammatory bowel disease, systemic lupus
CC erythematosus, ulcerative colitis, rheumatoid arthritis, Goodpasture's
CC syndrome, Grave's disease, Hashimoto's thyroiditis, pemphigus vulgaris,
CC myasthenia gravis, scleroderma, autoimmune hemolytic anemia, pernicious
CC anemia, Sjogren's syndrome, neurological disorders such as multiple
CC sclerosis, and inflammatory diseases or disorders such as cystic
CC fibrosis, sinusitis, gastroenteritis, drug reactions and burns. The
CC polypeptide is useful for diagnostic or therapeutic purposes. The binding
CC molecules are also useful for pretargeting applications for
CC chemotherapeutic drug delivery. The present sequence represents a light
CC chain variable region (optionally CH2 domain deleted) from the anti-Tag72
XX antibody huCC49.
SQ Sequence 220 AA;
Query Match 91.7%; Score 1140; DB 9; Length 220;
Best Local Similarity 100.0%; Pred. No. 6.1e-61;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKYNLAWYQKPGQSPKLLIYWASAR 80
DB 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKYNLAWYQKPGQSPKLLIYWASAR 60
QY 81 ESGVDPDRFSGSGGTDFTLTISVVQAEADVAVVYCOQYYSYPLTFGAGTKLEKRTVAAPS 140
DB 61 ESGVDPDRFSGSGGTDFTLTISVVQAEADVAVVYCOQYYSYPLTFGAGTKLEKRTVAAPS 120
QY 141 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 200
DB 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180
QY 201 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 240
DB 181 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 6
ADW50161
ID AAY50161 standard; protein; 240 AA.
XX AC AAY50161;
XX DT 17-OCT-2003 (revised)
XX DT 31-JAN-2000 (first entry)
XX DE Human reshaped F19 antibody light chain (version a).
```

XX Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;  
KW humanisation; complementarity determining region; CDR; CDR grafting;  
KW reshaped; reactive stroma; fibroblast; epithelial cancer; diagnosis;  
KW immune response; framework sequence; constant region; variable region;  
KW producibility; treatment; cancer; colorectal; lung; breast; head; neck;  
KW ovarian; lung; bladder; pancreatic; metastasis; detection; wound healing;  
KW skin inflammation; tumour; immunogenicity; chimeric; light chain.  
XX  
OS Mus sp.  
OS Homo sapiens.  
OS Chimeric.  
XX  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..20  
FT Protein /note= "Leader peptide"  
FT Protein 21..240  
FT Region /note= "Mature human reshaped F19 light chain"  
FT Region 21..140  
FT Region /note= "Mature reshaped human F19 light chain variable region"  
FT Region 44..60  
FT Region /note= "Complementarity determining region (CDR) 1"  
FT Region 76..82  
FT Region /note= "CDR 2"  
FT Region 115..123  
FT Region /note= "CDR 3"  
FT Region 141..240  
FT Region /note= "Human kappa light chain constant region"  
XX  
PN EP953639-A1.  
XX  
XX 03-NOV-1999.  
XX  
XX 30-APR-1998; 98EP-00107925.  
XX  
XX 30-APR-1998; 98EP-00107925.  
XX  
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
XX  
XX Park JE, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;  
XX Rettig WJ;  
XX  
XX WPI; 1999-G21833/54;  
XX N-PSDB; AA232784.  
XX  
XX New antibody protein, useful for treating cancer and for imaging presence  
XX of activated stromal fibroblasts in healing wound or inflamed skin.  
XX  
XX Example 3; Fig 30; 143pp; English.  
XX  
XX This sequence represents the light chain (version a) of a reshaped human  
XX F19 antibody. F19 (ATCC Accession number HB 8269) is a murine monoclonal  
XX antibody against fibroblast activation protein alpha (FAP). FAP is a cell  
XX surface molecule of reactive stromal fibroblasts, and its induction is a  
XX highly consistent molecular trait of the reactive stroma of many types of  
XX epithelial cancer. Although F19 may be useful in vitro, e.g., for  
XX diagnosis, its applications for in vivo use in humans are problematic as  
XX it elicits a human anti-mouse response which reduces the efficacy of the  
XX antibody in patients and impairs continued administration. The novel  
XX human reshaped F19 was humanised by grafting the murine complementarity  
XX determining regions (CDRs) of F19 onto human variable region framework  
XX sequences, and then joining these "reshaped human" variable regions to  
XX human constant regions. These modifications also result in the improved  
XX producibility in eukaryotic cell culture systems as compared to a  
XX chimeric antibody having the entire variable regions of F19 joined to  
XX human constant regions. The human reshaped F19 antibody has low  
XX immunogenicity for humans and is useful for treating cancers e.g.,  
XX colorectal cancers, non-small cell lung cancers, breast cancers, head and  
XX neck cancers, ovarian cancers, lung cancers, bladder cancers, pancreatic  
XX cancers and metastatic cancers. It is also useful for the detection of  
XX activated stromal fibroblasts in a healing wound, inflamed skin or a  
XX tumour in a human patient. (Updated on 17-OCT-2003 to standardise OS

CC field)  
XX  
SQ Sequence 240 AA;  
Query Match 91.4%; Score 1136; DB 2; Length 240;  
Best Local Similarity 90.0%; Pred. No. 1.1e-60;  
Matches 216; Conservative 12; Mismatches 12; Indels 0; Gaps 0;  
QY 1 MDSQAQVLMALLLWVSGTCGDIVMSQSPDSLAVSLGERTVLTNCKSSQSLYSNQKNYLA 60  
DB 1 METDTLLWVLLWVPGSGDIVMTQSPDSLAVSLGERATINCKSSQSLYSNQKNYLA 60  
QY 61 WYQOKPGQSPKLLIYWASRESCVPRFSGSGSGTDTFTLTISVQAEADVAVYVCOQYYSY 120  
DB 61 WYQOKPGQPPKLLIFWASTRESGVPDRFSGSGFGTDTFTLTISLQAEADVAVYVCOQYFSY 120  
QY 121 PLTFGAGTKLELKRITVAAPSVFIFPPSDEQLKSGTASVIVCLLNNFYPREAKVQWKVDNAL 180  
DB 121 PLTFGGGTVKEIKRTVAAPSVFIFPPSDEQLKSGTASVIVCLLNNFYPREAKVQWKVDNAL 180  
QY 181 QSGNSQESVTEQDSKDSYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
DB 181 QSGNSQESVTEQDSKDSYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
RESULT 7  
ADW77054  
ID ADW77054 standard; protein; 220 AA.  
XX  
AC ADW77054;  
XX  
XX 24-MAR-2005 (first entry)  
XX  
XX Light chain CH2 domain-deleted huCC49 polypeptide #2.  
XX  
XX Protein production; protein purification; cancer; lymphoma;  
KW autoimmune disease; inflammation; Crohns disease;  
KW inflammatory bowel disease; systemic lupus erythematosus;  
KW ulcerative colitis; rheumatoid arthritis; Goodpasture's syndrome;  
KW Grave's disease; Hashimoto's disease; pemphigus vulgaris;  
KW myasthenia gravis; scleroderma; autoimmune hemolytic anemia;  
KW pernicious anemia; Sjogrens syndrome; immunosuppressive; antianemic;  
KW dermatological; muscular-gen.; neuroprotective; thyromimetic;  
KW antithyroid; nephrotropic; antirheumatic; antiarthritic;  
KW antiinflammatory; antiulcer; gastrointestinal-gen.; neoplasm;  
KW immune disorder; huCC49; light chain; antibody.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX WO2005000898-A2.  
XX  
XX 06-JAN-2005.  
XX  
XX 28-JUN-2004; 2004WO-US020944.  
XX  
XX 27-JUN-2003; 2003US-0483877P.  
XX 03-OCT-2003; 2003US-0508810P.  
XX 28-OCT-2003; 2003US-0515151P.  
XX 30-OCT-2003; 2003US-0516030P.  
XX  
XX (BIOG-) BIOGEN IDEC MA INC.  
XX  
XX Braslawsky GR, Glaser S, Yang T, Hopp J, Chinn P;  
XX WPI; 2005-058132/06.  
XX N-PSDB; ADW77052.  
XX  
XX New composition comprising polypeptide dimers having at least two binding  
XX sites and at least two polypeptide chains comprising a heavy chain  
XX portion and a synthetic peptide, useful for treating e.g., cancer or  
XX autoimmune diseases.  
XX

PS Claim 31; SEQ ID NO 27; 152pp; English.

XX The invention relates to a composition comprising polypeptide dimers

CC having at least two binding sites and at least two polypeptide chains,

CC where the polypeptide chains comprise at least one heavy chain portion

CC and a synthetic connecting peptide. The invention also relates to a

CC nucleic acid molecule comprising a nucleotide sequence encoding a

CC polypeptide chain, a host cell comprising the nucleic acid molecule, a

CC connecting peptide, a domain deleted antibody molecule, an antibody

CC molecule, a method of separating a first properly folded antibody

CC molecule from a second improperly folded antibody molecule, where each of

CC the first and second antibody molecules comprises four polypeptide

CC chains, where at least two of the chains comprise at least one heavy

CC chain portion, and at least two of the chains comprise at least one light

CC chain portion, a method of increasing the amount of a first polypeptide

CC dimer relative to the amount of a second polypeptide dimer produced by a

CC cell, a composition comprising a first polypeptide dimer, a polypeptide

CC comprising a synthetic connecting peptide, where the polypeptide is not a

CC naturally occurring IgG3 molecule, and a method of increasing the amount

CC of dimers comprising polypeptide chains linked via at least one disulfide

CC linkage in a population of IgG4 molecules produced by a cell. The

CC composition is useful for treating a subject that would benefit from

CC treatment with a binding molecule, where the subject is suffering from

CC cancer, lymphoma, an autoimmune disease or disorder or an inflammatory

CC disease or disorder. The autoimmune diseases include Crohns disease,

CC inflammatory bowel disease, systemic lupus erythematosus, ulcerative

CC colitis, rheumatoid arthritis, Goodpasture's syndrome, Grave's disease,

CC Hashimoto's disease, pemphigus vulgaris, myasthenia gravis, scleroderma,

CC autoimmune hemolytic anemia, pernicious anemia and Sjogrens syndrome.

CC This sequence represents a light chain CH2 domain-deleted huCC49

CC polypeptide, used in the scope of the invention.

XX

SEQ Sequence 220 AA;

Query Match 91.3%; Score 1135; DB 9; Length 220;

Best Local Similarity 99.5%; Pred. No. 1.2e-60;

Matches 219; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 DIVMSGPSPLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQQKPGQPKLLIYWASAR 80

DB 1 DIVMSGPSPLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQQKPGQPKLLIYWASAR 60

QY 81 ESGVDPFRFSGSGGDTFTLTISVQAEADVAVVYCOQYYSYPLTFGAGTKLELKRITVAAPS 140

DB 61 ESGVDPFRFSGSGGDTFTLTISVQAEADVAVVYCOQYYSYPLTFGAGTKLELKRITVAAPS 120

QY 141 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYTS 200

DB 121 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYTS 180

QY 201 LSSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC 240

DB 181 LSSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 8

ADW23408

ID ADW23408 standard; protein; 240 AA.

XX ADW23408;

AC ADW23408;

DT 07-APR-2005 (first entry)

DE Human L612L protein.

XX immunoglobulin M; IgM; IgM H chain; IgM L chain; IgM J chain;

KW immunostimulatory; cytostatic; anti-HIV; cancer;

KW acquired immunodeficiency syndrome; L612L.

XX Homo sapiens.

OS W02005005636-A1.

XX

PD 20-JAN-2005.

XX

PF 15-JUL-2004; 2004WO-JP010444.

XX

PR 15-JUL-2003; 2003US-0487333P.

XX

PA (CHUS ) CHUGAI SEIYAKU KK.

PA (IRIE/) IRIE R.

PI Irie R, Teunoda H, Igawa T, Sekimori Y, Tsuchiya M;

DR WPI; 2005-122424/13.

XX N-PSDB; ADW23407.

XX New transformed Chinese hamster ovarian cell producing a specific amount

PT of immunoglobulin M, for use in treating a tumor or acquired

PT immunodeficiency syndrome.

XX

PS Claim 35; SEQ ID NO 4; 132pp; Japanese.

XX This invention describes a novel method for producing a transformed cell

CC capable of producing 100 mg/l or 35 or more pg/cell/day of immunoglobulin

CC M (IgM). Pentamer IgM is obtained by locating the IgM H chain, L chain or

CC J chain on a single vector and transforming the vector into an

CC appropriate host cell from a mammalian cell line. Substantially pure IgM

CC is obtained by purifying IgM from the culture supernatant of the cell

CC culture product. The gene encoding the J chain may be transferred via

CC cotransformation. If the J chain is not expressed the product is obtained

CC as hexamer IgM. The transformant obtained shows a high IgM productivity.

CC The invention also describes a method whereby a polymer IgM can be

CC separated and quantified. The products of the invention are

CC immunostimulatory and have cytostatic and anti-HIV activity. The purified

CC IgM can be used to treat or prevent cancer or acquired immunodeficiency

CC syndrome (AIDS). This sequence represents the human IgM associated

CC polypeptide, L612L.

XX

SEQ Sequence 240 AA;

Query Match 91.1%; Score 1132; DB 9; Length 240;

Best Local Similarity 91.1%; Pred. No. 2e-60;

Matches 216; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 4 QAOVLMLLLVSGTGGDIWMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQ 63

DB 4 QTOVFISLLLWISGAYGDIWMTQSPDSLAVSLGERATINCKSSQSLVYSSNNKNYLAWYQ 63

QY 64 QKPGSPKLLIYWASARESGVDPFRFSGSGGDTFTLTISVQAEADVAVVYCOQYYSYPLT 123

DB 64 QKPGQPKLLIYWASTRESGVDPFRFSGSGGDTFTLTISVQAEADVAVVYCOQYYSYPT 123

QY 124 FGAGTKLELKRITVAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 183

DB 124 FGQGTKEIKRTVAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 183

QY 184 NSQESVTEQDSKDSYTSLSSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC 240

DB 184 NSQESVTEQDSKDSYTSLSSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 9

ADZ51047

ID ADZ51047 standard; protein; 240 AA.

XX ADZ51047;

XX

DT 30-JUN-2005 (first entry)

XX Amino acid sequence of protein #2.

XX immunoglobulin M; IgM; multi-valent cationic ion; Magnesium chloride;

KW arginine hydrochloride.

XX Unidentified.

OS



```
XX PN WO2005035574-A1.
XX PD 21-APR-2005.
XX PF 08-OCT-2004; 2004WO-JP014935.
XX PR 09-OCT-2003; 2003JP-00351388.
XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX PI Igawa T, Sekimori Y;
XX WPI; 2005-315547/32.
XX DR N-PSDB; ADZ51046.
XX PT Stabilized solution, useful for preparing a stable pharmaceutical
XX PT composition containing immunoglobulin (IgM, comprises a high
XX PT concentration of immunoglobulin IgM.
XX PS Example 6; SEQ ID NO 4; 44pp; Japanese.
XX CC The specification describes a stabilized solution of high concentration
XX CC immunoglobulin M (IgM). The use of a multi-valent cationic ion, such as
XX CC magnesium chloride or arginine hydrochloride, as an additive allows
XX CC inhibition of the association of IgM in a solution. The present sequence
XX CC represents a protein, and is used in the course of the invention.
XX SQ Sequence 240 AA;
XX Query Match 91.1%; Score 1132; DB 9; Length 240;
XX Best Local Similarity 91.1%; Pred. No. 2e-60;
XX Matches 216; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
QY 4 QRAQLMLLLVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLYSNGKNYLAWYQ 63
DB 4 QTVFISLLWISGAYGDIVMTQSPDSLAVSLGERATINCKSSQSLYSNNKNYLAWYQ 63
QY 64 QKPGQPKLLIYWASARESGVDPFRFSGSGTDFTLTISVQAEADVAVYCCQYYSTPPT 123
DB 64 QKFGQPKLLIYWASTRESGVDPFRFSGSGTDFTLTISLQAEADVAVYCCQYYSTPPT 123
QY 124 FQAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 183
DB 124 FQGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 183
QY 184 NSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 240
DB 184 NSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 240
RESULT 10
ADZ56181
ID ADZ56181 standard; protein; 240 AA.
XX AC ADZ56181;
XX 30-JUN-2005 (first entry)
XX DE Protein stabilization method-related protein - SEQ ID 4.
XX KW protein stabilization; pharmaceutical.
XX OS Unidentified.
XX PN WO2005035573-A1.
XX PD 21-APR-2005.
XX PF 08-OCT-2004; 2004WO-JP014919.
XX PI Irie R, Tsunoda H, Igawa T, Sekimori Y, Tsuchiya M;
XX WO2005035574-A1.
```

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PA (CHUS ) CHUGAI SEIYAKU KK.
XX Hayasaka A, Igawa T, Sekimori Y;
XX WPI; 2005-315546/32.
XX DR N-PSDB; ADZ56180.
XX PT Stabilizing IgM protein from low temperature precipitation, by adding
XX PT citrate buffer solution to solution containing protein.
XX PS Example 3; SEQ ID NO 4; 31pp; Japanese.
XX CC The invention comprises a method of stabilizing a protein from a low
XX CC temperature precipitation, the method involves adding citrate buffer to
XX CC the solution containing the protein. The method of the invention is
XX CC useful for stabilizing protein from a low temperature precipitation and
XX CC in producing stable pharmaceutical compositions containing IgM. The
XX CC present amino acid sequence represents a protein that was used in an
XX CC example of the invention. NOTE: The present sequence is not shown in the
XX CC specification, but has been retrieved from the WIPO website.
XX SQ Sequence 240 AA;
XX Query Match 91.1%; Score 1132; DB 9; Length 240;
XX Best Local Similarity 91.1%; Pred. No. 2e-60;
XX Matches 216; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
QY 4 QRAQLMLLLVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLYSNGKNYLAWYQ 63
DB 4 QTVFISLLWISGAYGDIVMTQSPDSLAVSLGERATINCKSSQSLYSNNKNYLAWYQ 63
QY 64 QKPGQPKLLIYWASARESGVDPFRFSGSGTDFTLTISVQAEADVAVYCCQYYSTPPT 123
DB 64 QKFGQPKLLIYWASTRESGVDPFRFSGSGTDFTLTISLQAEADVAVYCCQYYSTPPT 123
QY 124 FQAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 183
DB 124 FQGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 183
QY 184 NSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 240
DB 184 NSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 240
RESULT 11
ADW23426
ID ADW23426 standard; protein; 241 AA.
XX AC ADW23426;
XX 07-APR-2005 (first entry)
XX DE Human L55L protein.
XX KW immunoglobulin M; IgM; IgM H chain; IgM L chain; IgM J chain;
XX KW immunostimulatory; cytostatic; anti-HIV; cancer;
XX KW acquired immunodeficiency syndrome; L55L.
XX OS Homo sapiens.
XX PN WO2005005636-A1.
XX PD 20-JAN-2005.
XX PF 15-JUL-2004; 2004WO-JP010444.
XX PR 15-JUL-2003; 2003US-0487333P.
XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX PA (IRIE/) IRIE R.
XX PI Irie R, Tsunoda H, Igawa T, Sekimori Y, Tsuchiya M;
XX WO2005005636-A1.
```

DR WPI: 2005-122424/13.  
 DR N-PSDB; ADW23425.  
 XX  
 PT New transformed Chinese hamster ovarian cell producing a specific amount  
 PT of immunoglobulin M, for use in treating a tumor or acquired  
 PT immunodeficiency syndrome.  
 XX  
 XX  
 PS Claim 42; SEQ ID NO 22; 132pp; Japanese.  
 XX  
 CC This invention describes a novel method for producing a transformed cell  
 CC capable of producing 100 mg/l or 35 or more pg/cell/day of immunoglobulin  
 CC M (IgM). Pentamer IgM is obtained by locating the IgM H chain, L chain or  
 CC J chain on a single vector and transforming the vector into an  
 CC appropriate host cell from a mammalian cell line. Substantially pure IgM  
 CC is obtained by purifying IgM from the culture supernatant of the cell  
 CC culture product. The gene encoding the J chain may be transferred via  
 CC cotransformation. If the J chain is not expressed the product is obtained  
 CC as hexamer IgM. The transformant obtained shows a high IgM productivity.  
 CC The invention also describes a method whereby a polymer IgM can be  
 CC separated and quantified. The products of the invention are  
 CC immunostimulatory and have cytostatic and anti-HIV activity. The purified  
 CC IgM can be used to treat or prevent cancer or acquired immunodeficiency  
 CC syndrome (AIDS). This sequence represents the human IgM associated  
 CC polypeptide, L55L.  
 XX  
 SQ Sequence 241 AA;

Query Match 90.7%; Score 1127.5; DB 9; Length 241;  
 Best Local Similarity 90.8%; Pred. No. 3.7e-60;  
 Matches 216; Conservative 9; Mismatches 12; Indels 1; Gaps 1;  
 QY 4 QAOVLMLLLWVSGTCDIVMSQSPDSLAVSLGERTVLTNCKSSQSLLYSGNQKNYLA 63  
 DB 4 QTQVFISLLWTSGAYGDTVMTQSPDSLAVSLGERATINCKSSQSLYSSNNKNYLA 63  
 QY 64 QKPGQSPKLLIYWASARESGVDPDRFSGSGGTDFLTITSSVQAEADVAVYCOQY-SYPL 122  
 DB 64 QKPGQSPKLLIYWASTRESGVDPDRFSGSGGTDFLTITSSVQAEADVAVYCOQY 123  
 QY 123 TFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 182  
 DB 124 TFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 183  
 QY 183 GNSQSVTEQDSKDYSLSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
 DB 184 GNSQSVTEQDSKDYSLSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 241

RESULT 12  
 ADV92470  
 ID ADV92470 standard; protein; 239 AA.  
 XX  
 AC ADV92470;  
 XX  
 DT 10-MAR-2005 (first entry)  
 XX  
 DE SM5-1 chimeric antibody (ChSM) light chain protein.  
 XX  
 KW Antibody engineering; chimeric antibody; cytostatic; gene therapy;  
 KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;  
 KW breast cancer; hepatocellular carcinoma.  
 XX  
 OS Homo sapiens.  
 OS Mus sp.  
 OS Chimeric.  
 XX  
 FH Key  
 FT Peptide  
 FT Peptide  
 FT Protein  
 FT Protein  
 FT Protein  
 FT Region

Location/Qualifiers  
 1..20  
 /label= Signal peptide  
 21..239  
 /notes= "Mature SM5-1 chimeric antibody (ChSM) light chain protein"  
 21..133

FT Region /note= "Light chain variable region gene (VL)"  
 FT 134..239  
 FT /note= "Human kappa chain constant cDNA (CL)"  
 XX  
 PN US2004254108-A1.  
 XX 16-DEC-2004.  
 XX 26-NOV-2003; 2003US-00723003.  
 XX 13-JUN-2003; 2003CN-00129290.  
 XX 25-NOV-2003; 2003CN-01119930.  
 XX (MAJJ/) MA J.  
 XX (GUOY/) GUO Y.  
 XX Ma J, Guo Y;  
 XX WPI: 2005-030218/03.  
 XX N-PSDB; ADV92469.  
 XX New chimeric protein comprises an Flt3 ligand and a proteinous or  
 PT peptidyl tumoricidal agent, useful for treating malignancy or neoplasm,  
 PT e.g. melanoma, breast cancer, or hepatocellular carcinoma.  
 XX  
 PS Example 3; SEQ ID NO 14; 158pp; English.  
 XX  
 CC The present invention relates to a chimeric protein having a Flt3 ligand  
 CC (FL) or its biologically active fragment and a proteinous or peptidyl  
 CC tumoricidal agent. The invention is useful for treating malignancy,  
 CC neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a  
 CC vaccine for eliciting an immune response. The invention is also useful in  
 CC gene therapy. The present sequence is the SM5-1 chimeric antibody (ChSM)  
 CC light chain protein.  
 XX  
 SQ Sequence 239 AA;

Query Match 90.5%; Score 1125.5; DB 9; Length 239;  
 Best Local Similarity 89.6%; Pred. No. 4.9e-60;  
 Matches 215; Conservative 13; Mismatches 11; Indels 1; Gaps 1;  
 QY 1 MDSQAOVLMLLLWVSGTCDIVMSQSPDSLAVSLGERTVLTNCKSSQSLLYSGNQKNYLA 60  
 DB 1 MESQTQVFLSLLWVSGTCGIMMTQSPDSLAVSAGEKVTMCKSSQSLYSSNQKNYLA 60  
 QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDFLTITSSVQAEADVAVYCOQY 120  
 DB 61 WYQKPGQSPKLLIYWASTRESGVDPDRFTGSGSGGTDFLTITSSVQAEADVAVYCHQYFS- 119  
 QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 180  
 DB 120 SYTFGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 179  
 QY 181 QSGNSQSVTEQDSKDYSLSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
 DB 180 QSGNSQSVTEQDSKDYSLSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 13  
 ADV98533  
 ID ADV98533 standard; protein; 239 AA.  
 XX  
 AC ADV98533;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX  
 DE Novel chimeric protein-related ChSM light chain protein SeqID14.  
 XX  
 KW protein engineering; pharmaceutical; cytostatic; vaccine; cancer;  
 KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.  
 XX  
 OS Mus sp.  
 OS Synthetic.

XX WO2005001048-A2.  
XX 06-JAN-2005.  
XX 04-JUN-2004; 2004WO+US017765.  
XX 13-JUN-2003; 2003CN+00129290.  
XX 25-NOV-2003; 2003CN-01119930.  
XX 26-NOV-2003; 2003US-00723003.  
XX 28-NOV-2003; 2003TW+00133577.  
XX (SYMB-) SYMBIGENE ACQUISITION CO INC.  
XX Ma J, Guo Y;  
XX WPI: 2005-075540/08;  
XX N-PSDB; ADV98532.  
XX New chimeric protein for preventing or treating neoplastic conditions,  
XX e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an  
XX Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal  
XX agent.  
XX Example 3; Fig 9; 147pp; English.  
XX This invention relates to a novel chimeric protein comprising an Flt3  
XX ligand, or its biological fragment, and a proteinous or peptidyl  
XX tumoricidal agent. The invention may be useful for the production of  
XX compounds with a cytostatic activity or a vaccine. The composition and  
XX methods are useful for preventing or treating neoplastic conditions, such  
XX as melanoma, breast cancer or hepatocellular carcinoma. The present  
XX sequence is that of a protein which is related to the chimeric proteins  
XX of the invention. Note: Two sequences were allocated this SeqID number in  
XX the specification, the alternative sequence is shown on page 21.  
XX Sequence 239 AA;  
XX  
XX Query Match 90.5%; Score 1125.5; DB 9; Length 239;  
XX Best Local Similarity 89.6%; Pred. No. 4.9e-60;  
XX Matches 215; Conservative 13; Mismatches 11; Indels 1; Gaps 1;  
QY 1 MDSQAQVLMILLVWVGTCGDIVMSQSPSLAVSLGERTVLNCKSSQSLYSGNQKXYLA 60  
Db 1 MESQTQVFLSLILWVGTCGCTNMTQSPSSLAVSAGEKVTMCKSSQSLYSSNQKXYLA 60  
QY 61 WYQKPGQSPKLLIYWASRESGVPRFSGSGGTDFTLTISVQAEDVAVVYCCQYYSV 120  
Db 61 WYQKPGQSPKLLIYWASRESGVPRFSGSGGTDFTLTISVQAEDVAVVYCHQYFS- 119  
QY 121 PLTFGAGTKLEKRTVAAPSVFPPSPDLQSGTASVCLLNFFYPREAKVQWKVDNAL 180  
Db 120 SYTFGGTKLEIKRTVAAPSVFPPSPDLQSGTASVCLLNFFYPREAKVQWKVDNAL 179  
QY 181 QSGNSQESVTEQDSKDYSLSTLTLSKADYKEKHVYACEVTHQGLSSPVTKSFNRGRC 240  
Db 180 QSGNSQESVTEQDSKDYSLSTLTLSKADYKEKHVYACEVTHQGLSSPVTKSFNRGRC 239  
RESULT 14  
AAU00815  
ID AAU00815 standard; protein; 240 AA.  
XX  
XX AAU00815;  
XX  
XX 01-JUN-2001 (first entry)  
XX Human Immunoglobulin superfamily, IgSF, protein #1.  
XX Human; Immunoglobulin superfamily protein; IgSF; Immune response;  
KW inflammatory response; cell-cell interaction; cell-surface recognition;  
KW neural disorder; immune system disorder; muscular disorder;  
KW reproductive disorder; gastrointestinal disorder; pulmonary disorder;  
KW

KW cardiovascular disorder; renal disorder; proliferative disorder; cancer;  
KW common variable deficiency syndrome; AIDS; SCID;  
KW acquired immunodeficiency syndrome; anaemia; rheumatoid arthritis;  
KW Alzheimer's disease; Crohn's disease; liver cancer; leukaemia;  
KW Hodgkin's lymphoma; Parkinson's disease; Huntington's disease; dementia;  
KW arteriosclerosis; stroke; diabetes mellitus; Addison's disease;  
KW urticaria; severe combined immunodeficiency; antibody.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Region 52..58  
XX /label= Immunogenic\_epitope  
XX Region 63..70  
XX /label= Immunogenic\_epitope  
XX Region 79..90  
XX /label= Immunogenic\_epitope  
XX Region 118..126  
XX /label= Immunogenic\_epitope  
XX Region 146..154  
XX /label= Immunogenic\_epitope  
XX Domain 160..240  
XX /label= Immunoglobulin\_like\_domain  
XX Region 183..199  
XX /label= Immunogenic\_epitope  
XX Region 209..215  
XX /label= Immunogenic\_epitope  
XX Region 233..240  
XX /label= Immunogenic\_epitope  
XX WO200118176-A1.  
XX 15-MAR-2001.  
XX 29-AUG-2000; 2000WO-US023662.  
XX 03-SEP-1999; 99US-0152248P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (NIJ/) NI J.  
XX Young PE, Ruben SM, Shi Y;  
XX WPI: 2001-203084/20.  
XX N-PSDB; AAS00145.  
XX Isolated nucleic acid molecule encoding a human secreted protein is used  
XX in preventing, treating or ameliorating a medical condition.  
XX Claim 11; Page 237; 247pp; English.  
XX The sequence is a Human Immunoglobulin superfamily, IgSF, protein, a  
XX diverse family of proteins involved in cell-cell interactions, cell-  
XX surface recognition, intercellular communication and immune and  
XX inflammatory responses. Polypeptides and antibodies directed to  
XX polypeptides of the present invention are useful to provide immunological  
XX probes for differential identification of tissues. Antibodies can be used  
XX to assay levels of polypeptides encoded by polynucleotides of the  
XX invention. Polypeptides of the present invention can be used to treat or  
XX prevent diseases or conditions such as neural disorders, immune system  
XX disorders, muscular disorders, reproductive disorders, gastrointestinal  
XX disorders, pulmonary disorders, cardiovascular disorders, renal  
XX disorders, proliferative disorders, and/or cancerous diseases and  
XX conditions. Polynucleotides of the invention are also useful in treating  
XX the above disorders. Examples of the disorders include common variable  
XX adhesion deficiency syndrome, acquired immunodeficiency syndrome (AIDS),  
XX anaemia, rheumatoid arthritis, Alzheimer's disease, Crohn's disease,  
XX liver cancer, leukaemia, Hodgkin's lymphoma, Parkinson's disease,  
XX Huntington's disease, dementia, arteriosclerosis, stroke, diabetes  
XX mellitus, Addison's disease, urticaria, severe combined immunodeficiency  
XX (SCID). Many more examples of diseases and disorders are given in the  
XX specification  
XX

SQ Sequence 240 AA;  
Query Match 90.5%; Score 1125; DB 4; Length 240;  
Best Local Similarity 90.3%; Pred. No. 5.2e-60;  
Matches 214; Conservative 10; Mismatches 13; Indels 0; Gaps 0;  
QY 4 QAOVLMLLLWVSGTCGDIWMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 63  
DB 4 QTVFISLLWLTSGAYGDIWMTQSPDSLAVSLGERATINCKSQTVLYSSDNKNYLA 63  
QY 64 QKPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFTLTISVQAEDVAVVYCCQYYSYPLT 123  
DB 64 QKPGQSPKLLIYWASTRESGVDPDRFSGSGSGTDFTLTISVQAEDVAVVYCCQYYSYPLT 123  
QY 124 FQAGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQSG 183  
DB 124 FQAGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQSG 183  
QY 184 NSQESVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
DB 184 NSQESVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 15  
ADJ65029  
ID ADJ65029 standard; protein; 240 AA.  
AC ADJ65029;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Plasmid pD16-H39E3.L1 light chain antibody amino acid sequence SEQ:8.  
XX  
KW humanised antibody; human 4-1BB; human 4-1BB ligand; cancer; cytostatic;  
KW gene therapy; antibody; plasmid; pD16-H39E3.L1.  
XX  
OS Synthetic.  
XX  
FN WO2004010947-A2.  
XX  
PD 05-FEB-2004.  
XX  
PF 30-JUL-2003; 2003WO-US023735.  
XX  
PR 30-JUL-2002; 2002US-0399646P.  
XX  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
PI Jure-Kunkel M, Ganguly S, Abraham R, Hollenbaugh DL, Rillema J;  
PI Thorne B, Shuford WW, Mittler RS;  
XX  
DR WPI; 2004-143726/14.  
DR N-PSDB; ADJ65027.  
XX  
PT New humanized antibody that binds to human 4-1BB and allows binding of  
PT human 4-1BB to a human 4-1BB ligand, useful for preparing a composition  
PT for treating cancer.  
XX  
PS Claim 4; SEQ ID NO 8; 78pp; English.  
XX  
CC The present invention describes a humanised antibody (I) that binds to  
CC human 4-1BB and allows binding of human 4-1BB to a human 4-1BB ligand.  
CC Also described: (1) a pharmaceutical composition comprising the antibody  
CC (I) and a carrier; (2) treating cancer in a subject; and (3) an isolated  
CC polynucleotide comprising nucleotides 693-2072 of the 7033-base pairs  
CC (bp) sequence (SEQ ID NO: 3, ADJ65024) or nucleotides 633-1034 or 1409-  
CC 1726 of the 8874-bp sequence (SEQ ID NO: 6, ADJ65027). (I) has cytostatic  
CC activity, and can be used in gene therapy. The humanised antibody (I) can  
CC be used for preparing a composition for treating cancer. The present  
CC sequence represents the plasmid pD16-H39E3.L1 light chain antibody amino  
CC acid sequence, which is used in an example from the present invention.  
XX  
SQ Sequence 240 AA;

Query Match 90.3%; Score 1122; DB 8; Length 240;  
Best Local Similarity 90.0%; Pred. No. 7.9e-60;  
Matches 216; Conservative 10; Mismatches 14; Indels 0; Gaps 0;  
QY 1 MDSQAQVLMLLWVSGTCGDIWMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 60  
DB 1 MEAPAQLLFLLLLWLPDITGDIWMTQSPDSLAVSLGERATINCKSSQSLLYSGNQKNYLA 60  
QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFTLTISVQAEDVAVVYCCQYYSY 120  
DB 61 WYQKPGQSPKLLIYASTRQSGVDPDRFSGSGSGTDFTLTISVQAEDVAVVYCCQYDRY 120  
QY 121 PLTFGAGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNAL 180  
DB 121 PFTFGQGTLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNAL 180  
QY 181 QSGNSQESVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
DB 181 QSGNSQESVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240

Search completed: February 16, 2006, 10:17:41  
Job time : 134.121 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 16, 2006, 10:39:32 ; Search time 13.1111 Seconds  
(without alignments)  
383.795 Million cell updates/sec

Title: US-10-058-069-7

Perfect score: 1876

Sequence: 1 MGWSLLFLVAVATRVLSQ.....MHEALHHYQKSLSLSPK 354

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications\_AA\_New.\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
  - 7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1632	87.0	462	7	US-11-177-648-30 Sequence 30, Appl
2	1630	86.9	462	7	US-11-177-648-97 Sequence 97, Appl
3	1629	86.8	462	7	US-11-177-648-29 Sequence 29, Appl
4	1629	86.8	462	7	US-11-177-648-32 Sequence 32, Appl
5	1628	86.8	462	7	US-11-177-648-96 Sequence 96, Appl
6	1627	86.7	462	7	US-11-177-648-95 Sequence 95, Appl
7	1626	86.7	462	7	US-11-177-648-33 Sequence 33, Appl
8	1624	86.6	462	7	US-11-177-648-31 Sequence 31, Appl
9	1624	86.6	462	7	US-11-177-648-94 Sequence 94, Appl
10	1622	86.5	462	7	US-11-177-648-93 Sequence 93, Appl
11	1621	86.4	462	7	US-11-177-648-92 Sequence 92, Appl
12	1619	86.3	462	7	US-11-177-648-27 Sequence 27, Appl
13	1616	86.1	462	7	US-11-177-648-28 Sequence 28, Appl
14	1614	86.0	462	7	US-11-177-648-98 Sequence 98, Appl
15	1612	85.9	462	7	US-11-177-648-26 Sequence 26, Appl
16	1608	85.7	462	7	US-11-177-648-79 Sequence 79, Appl
17	1599	85.2	462	7	US-11-177-648-9 Sequence 9, Appl
18	1566.5	83.5	467	7	US-11-158-505-72 Sequence 72, Appl
19	1565.5	83.4	467	7	US-11-158-505-5 Sequence 5, Appl
20	1565.5	83.4	467	7	US-11-158-505-7 Sequence 7, Appl
21	1565.5	83.4	467	7	US-11-158-505-13 Sequence 13, Appl
22	1565.5	83.4	467	7	US-11-158-505-15 Sequence 15, Appl
23	1565.5	83.4	467	7	US-11-158-505-21 Sequence 21, Appl
24	1565.5	83.4	467	7	US-11-158-505-23 Sequence 23, Appl
25	1565.5	83.4	467	7	US-11-158-505-29 Sequence 29, Appl

ALIGNMENTS

RESULT 1

US-11-177-648-30  
; Sequence 30, Application US/11177648  
; Publication No. US20060029603A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonathon Henry ELLIS  
; APPLICANT: Paul Andrew HAMBLIN  
; APPLICANT: Paul Alexander WILSON  
; APPLICANT: Alan Peter LEWIS  
; TITLE OF INVENTION: IMMUNOGLOBULINS  
; FILE REFERENCE: PB60608-2  
; CURRENT APPLICATION NUMBER: US/11/177,648  
; CURRENT FILING DATE: 2005-07-06  
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325  
; PRIOR FILING DATE: 2004-12-20  
; PRIOR APPLICATION NUMBER: GB0329711.6  
; PRIOR FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: GB0329684.5  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 2A10 heavy chain humanised construct H15  
US-11-177-648-30

Query Match 87.0%; Score 1632; DB 7; Length 462;

Best Local Similarity 69.2%; Pred. No. 3.2e-97;

Matches 321; Conservative 10; Mismatches 21; Indels 112; Gaps 2;

QY	1	MGWSLLFLVAVATRVLSQVLVQSGAEVVKPGASVKISCKASGYTFTDHAHWMVKQP	60
Db	1	MGWSLLFLVATATGVHSQVLVQSGAEVVKPGASVKISCKASGYTFTSYWHWVKQP	60
QY	61	GQRLEWIGVPSGNDFFKYNRFGKATLTADTSASTAYVELSLRSEDATVYFCTRSLN	120
Db	61	GQGLEWIGNPSGNGTNYNEFKSKATLTVDTSSTAYNELSLRSEDSAVYVC--ELG	118
QY	121	MAYWGQGLTVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGAL	180
Db	119	QGYWGQGLTVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGAL	178
QY	181	TSGVHTFPFVQLQSSGLYSLSVVTVPSSSLGTTOTYICNVNHPKSNTKVDKKVPKSCDKT	240
Db	179	TSGVHTFPFVQLQSSGLYSLSVVTVPSSSLGTTOTYICNVNHPKSNTKVDKKVPKSCDKT	238

QY 241 HTPCPCP----- 247  
|||  
Db 239 HTPCPCPAPELAGAPSVFLPPPKDTLMSRTPVTCVVVDVSHEDPEVKFNWYVDGVE 298  
|||  
QY 248 -----GQP 250  
|||  
Db 299 VHNAKTKPREEQYNSTYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKISKAKGQP 358  
|||  
QY 251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 310  
|||  
Db 359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 418  
|||  
QY 311 FFYLSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354  
|||  
Db 419 FFYLSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 462  
|||

## RESULT 2

US-11-177-648-97  
; Sequence 97, Application US/11177648  
; Publication No. US20060029603A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonathon Henry ELLIS  
; APPLICANT: Paul Andrew HAMBLIN  
; APPLICANT: Paul Alexander WILSON  
; APPLICANT: Alan Peter LEWIS  
; TITLE OF INVENTION: IMMUNOGLOBULINS  
; FILE REFERENCE: PB60608-2  
; CURRENT APPLICATION NUMBER: US/11/177,648  
; PRIOR FILING DATE: 2005-07-06  
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325  
; PRIOR FILING DATE: 2004-12-20  
; PRIOR APPLICATION NUMBER: GB0329711.6  
; PRIOR FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: GB0329684.5  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 97  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 2A10 heavy chain humanised construct H24  
US-11-177-648-97

Query Match 86.9%; Score 1630; DB 7; Length 462;  
Best Local Similarity 69.2%; Pred. No. 4.3e-97;  
Matches 321; Conservative 8; Mismatches 23; Indels 112; Gaps 2;  
  
QY 1 MGWSLILLFLVAVATRVLSQVLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWYKQP 60  
|||  
Db 1 MGWSLILLFLVAVATRVLSQVLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWYKQP 60  
|||  
QY 61 GQLEWIGYFSPGNDDFKYNRERFKGKATLTADTSASTAYVELSSLRSEDYAVYFCTRSLN 120  
|||  
Db 61 GQLEWIGININPNSGGTNYNEKFKSRATLTDRDTSTSTAYMELSSLRSEDYAVYVC--ELG 118  
|||  
QY 121 MAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 180  
|||  
Db 119 QGYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 178  
|||  
QY 181 TSGVHTFPVAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKT 240  
|||  
Db 179 TSGVHTFPVAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKT 238  
|||  
QY 241 HTPCPCP----- 247  
|||  
Db 239 HTPCPCPAPELAGAPSVFLPPPKDTLMSRTPVTCVVVDVSHEDPEVKFNWYVDGVE 298  
|||  
QY 248 -----GQP 250  
|||

Db 299 VHNAKTKPREEQYNSTYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKISKAKGQP 358  
|||  
QY 251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 310  
|||  
Db 359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 418  
|||  
QY 311 FFYLSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354  
|||  
Db 419 FFYLSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 462  
|||

## RESULT 3

US-11-177-648-29  
; Sequence 29, Application US/11177648  
; Publication No. US20060029603A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonathon Henry ELLIS  
; APPLICANT: Paul Andrew HAMBLIN  
; APPLICANT: Paul Alexander WILSON  
; APPLICANT: Alan Peter LEWIS  
; TITLE OF INVENTION: IMMUNOGLOBULINS  
; FILE REFERENCE: PB60608-2  
; CURRENT APPLICATION NUMBER: US/11/177,648  
; PRIOR FILING DATE: 2005-07-06  
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325  
; PRIOR FILING DATE: 2004-12-20  
; PRIOR APPLICATION NUMBER: GB0329711.6  
; PRIOR FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: GB0329684.5  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 2A10 heavy chain humanised construct H14  
US-11-177-648-29

Query Match 86.8%; Score 1629; DB 7; Length 462;  
Best Local Similarity 69.2%; Pred. No. 5e-97;  
Matches 321; Conservative 9; Mismatches 22; Indels 112; Gaps 2;  
  
QY 1 MGWSLILLFLVAVATRVLSQVLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWYKQP 60  
|||  
Db 1 MGWSLILLFLVAVATRVLSQVLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWYKQP 60  
|||  
QY 61 GQLEWIGYFSPGNDDFKYNRERFKGKATLTADTSASTAYVELSSLRSEDYAVYFCTRSLN 120  
|||  
Db 61 GQLEWIGININPNSGGTNYNEKFKSRATLTDRDTSTSTAYMELSSLRSEDYAVYVC--ELG 118  
|||  
QY 121 MAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 180  
|||  
Db 119 QGYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 178  
|||  
QY 181 TSGVHTFPVAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKT 240  
|||  
Db 179 TSGVHTFPVAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKT 238  
|||  
QY 241 HTPCPCP----- 247  
|||  
Db 239 HTPCPCPAPELAGAPSVFLPPPKDTLMSRTPVTCVVVDVSHEDPEVKFNWYVDGVE 298  
|||  
QY 248 -----GQP 250  
|||  
Db 299 VHNAKTKPREEQYNSTYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKISKAKGQP 358  
|||  
QY 251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 310  
|||  
Db 359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 418  
|||  
QY 311 FFYLSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354  
|||

Db 419 FFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 462

RESULT 4  
US-11-177-648-32  
; Sequence 32, Application US/11177648  
; Publication No. US20060029603A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonathon Henry ELLIS  
; APPLICANT: Paul Andrew HAMBLIN  
; APPLICANT: Paul Alexander WILSON  
; APPLICANT: Alan Peter LEWIS  
; TITLE OF INVENTION: IMMUNOGLOBULINS  
; FILE REFERENCE: PB60608-2  
; CURRENT APPLICATION NUMBER: US/11/177,648  
; CURRENT FILING DATE: 2005-07-06  
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325  
; PRIOR FILING DATE: 2004-12-20  
; PRIOR APPLICATION NUMBER: GB0329711.6  
; PRIOR FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: GB0329684.5  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 2A10 heavy chain humanised construct H17  
US-11-177-648-32

Query Match 86.8%; Score 1629; DB 7; Length 462;  
Best Local Similarity 69.2%; Pred. No. 5e-97;  
Matches 321; Conservative 8; Mismatches 23; Indels 112; Gaps 2;  
  
QY 1 MGNLSILLFLVAVATRVLSQVQLVQSGAEVVRPGASVKISKASGYTFTDHAHWHYKQP 60  
Db 1 MGNSCIILFLVATATGVHSQVQLVQSGAEVVRPGASVKISKASGYTFTSYNMHWYKQP 60  
  
QY 61 GQRLWIGVPSGNDDFKYNRERFKGKATLTADTSASTAYVELSSLRSEDYAVYFCTRSLN 120  
Db 61 GQGLEWIGNINPSNGGTNYNEKFKSKATLTVDKSTSTAYMELSSLRSEDYAVYIC--ELG 118  
  
QY 121 MAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 180  
Db 119 QGWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 178  
  
QY 181 TSGVHTFPFVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKT 240  
Db 179 TSGVHTFPFVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKT 238  
  
QY 241 HTCPPCP----- 247  
Db 239 HTCPPCPAPELAGAPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298  
  
QY 248 -----GQP 250  
Db 299 VHNAKTKPREEQNSTYRVSVLTVLHQDWLNGKEYKCKVKNKALPAPIEKTIISKAKGP 358  
  
QY 251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS 310  
Db 359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS 418  
  
QY 311 FFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 354  
Db 419 FFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 462

RESULT 5  
US-11-177-648-96  
; Sequence 96, Application US/11177648

; Publication No. US20060029603A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonathon Henry ELLIS  
; APPLICANT: Paul Andrew HAMBLIN  
; APPLICANT: Paul Alexander WILSON  
; APPLICANT: Alan Peter LEWIS  
; TITLE OF INVENTION: IMMUNOGLOBULINS  
; FILE REFERENCE: PB60608-2  
; CURRENT APPLICATION NUMBER: US/11/177,648  
; CURRENT FILING DATE: 2005-07-06  
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325  
; PRIOR FILING DATE: 2004-12-20  
; PRIOR APPLICATION NUMBER: GB0329711.6  
; PRIOR FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: GB0329684.5  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 96  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 2A10 heavy chain humanised construct H23  
US-11-177-648-96

Query Match 86.8%; Score 1628; DB 7; Length 462;  
Best Local Similarity 69.0%; Pred. No. 5.8e-97;  
Matches 320; Conservative 9; Mismatches 23; Indels 112; Gaps 2;  
  
QY 1 MGNLSILLFLVAVATRVLSQVQLVQSGAEVVRPGASVKISKASGYTFTDHAHWHYKQP 60  
Db 1 MGNSCIILFLVATATGVHSQVQLVQSGAEVVRPGASVKISKASGYTFTSYNMHWYKQP 60  
  
QY 61 GQRLWIGVPSGNDDFKYNRERFKGKATLTADTSASTAYVELSSLRSEDYAVYFCTRSLN 120  
Db 61 GQGLEWIGNINPSNGGTNYNEKFKSKATLTVDKSTSTAYMELSSLRSEDYAVYIC--ELG 118  
  
QY 121 MAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 180  
Db 119 QGWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 178  
  
QY 181 TSGVHTFPFVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKT 240  
Db 179 TSGVHTFPFVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKT 238  
  
QY 241 HTCPPCP----- 247  
Db 239 HTCPPCPAPELAGAPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298  
  
QY 248 -----GQP 250  
Db 299 VHNAKTKPREEQNSTYRVSVLTVLHQDWLNGKEYKCKVKNKALPAPIEKTIISKAKGP 358  
  
QY 251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS 310  
Db 359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS 418  
  
QY 311 FFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 354  
Db 419 FFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 462

RESULT 6  
US-11-177-648-95  
; Sequence 95, Application US/11177648  
; Publication No. US20060029603A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonathon Henry ELLIS  
; APPLICANT: Paul Andrew HAMBLIN  
; APPLICANT: Paul Alexander WILSON  
; APPLICANT: Alan Peter LEWIS  
; TITLE OF INVENTION: IMMUNOGLOBULINS



```
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H22
US-11-177-648-95

Query Match      86.7%; Score 1627; DB 7; Length 462;
Best Local Similarity 69.0%; Pred. No. 6,7e-97;
Matches 320; Conservative 9; Mismatches 23; Indels 112; Gaps 2;

QY 1 MCGSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60
Db 1 MCGSCILFLVATATGVHSQVQLVQSGAEVVKPGASVKISCKASGYTFISYWHVWKQRP 60

QY 61 GORLEWIGYFSPGNDDFKYNRPFKSKATLTADTSATAYVELSSLRSEDYAVYFCTRSLN 120
Db 61 GQGLEWIGNINPSNGGTNYNEKFKSKATLTVDKSSSTAYMELSSLRSEDSAVYVC--ELG 118

QY 121 MAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGAL 180
Db 119 QGYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGAL 178

QY 181 TSGVHTFPVAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKT 240
Db 179 TSGVHTFPVAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKT 238

QY 241 HTCPPCP-----247
Db 239 HTCPPCPAPELAGAPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298

QY 248 -----GQP 250
Db 299 VHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQP 358

QY 251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS 310
Db 359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS 418

QY 311 FFLYSKLTVDKSRWQOGNVFSCSVMEALHNNHYTKSLSPGK 354
Db 419 FFLYSKLTVDKSRWQOGNVFSCSVMEALHNNHYTKSLSPGK 462

RESULT 7
US-11-177-648-33
; Sequence 33, Application US/11/177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMELIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 462
; TYPE: PRT
```

```
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H18
US-11-177-648-33

Query Match      86.7%; Score 1626; DB 7; Length 462;
Best Local Similarity 69.0%; Pred. No. 7,7e-97;
Matches 320; Conservative 10; Mismatches 22; Indels 112; Gaps 2;

QY 1 MCGSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60
Db 1 MCGSCILFLVATATGVHSQVQLVQSGAEVVKPGASVKISCKASGYTFTSYWHVWKQRP 60

QY 61 GORLEWIGYFSPGNDDFKYNRPFKSKATLTADTSATAYVELSSLRSEDYAVYFCTRSLN 120
Db 61 GQGLEWIGNINPSNGGTNYNEKFKSKATLTVDKSSSTAYMELSSLRSEDSAVYVC--ELG 118

QY 121 MAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGAL 180
Db 119 QGYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGAL 178

QY 181 TSGVHTFPVAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKT 240
Db 179 TSGVHTFPVAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKT 238

QY 241 HTCPPCP-----247
Db 239 HTCPPCPAPELAGAPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298

QY 248 -----GQP 250
Db 299 VHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQP 358

QY 251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS 310
Db 359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS 418

QY 311 FFLYSKLTVDKSRWQOGNVFSCSVMEALHNNHYTKSLSPGK 354
Db 419 FFLYSKLTVDKSRWQOGNVFSCSVMEALHNNHYTKSLSPGK 462

RESULT 8
US-11-177-648-31
; Sequence 31, Application US/11/177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMELIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 462
; TYPE: PRT
```



; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: 2A10 heavy chain humanised construct H16

US-11-177-648-31

Query Match 86.6%; Score 1624; DB 7; Length 462;

Best Local Similarity 69.0%; Pred. No. 1e-96;

Matches 320; Conservative 8; Mismatches 24; Indels 112; Gaps 2;

QY 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWHVKQNP 60

DB 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTSYMHHVWRQP 60

QY 61 GQLEWIGVSPGNDPFKNRFGKATLTADTSASTAYVELSLRSEDVAVYFCTRSN 120

DB 61 GQLEWIGVSPGNDPFKNRFGKATLTADTSASTAYVELSLRSEDVAVYFCTRSN 120

QY 121 MAYWGQGLTVVSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGAL 180

DB 119 QGWGQGLTVVSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGAL 178

QY 181 TSGVHTFPFPAVLQSSGLYSLSVVTPSSSLGTQYICNVNHPKSNKTKVDKKVPEPKSCDKT 240

DB 179 TSGVHTFPFPAVLQSSGLYSLSVVTPSSSLGTQYICNVNHPKSNKTKVDKKVPEPKSCDKT 238

QY 241 HTCPPCP----- 247

DB 239 HTCPPCPAPELAGAPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298

QY 248 -----GQP 250

DB 299 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 358

QY 251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSDGS 310

DB 359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSDGS 418

QY 311 FFYLSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354

DB 419 FFYLSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 462

RESULT 9

US-11-177-648-94

; Sequence 94, Application US/11177648

; Publication No. US20060029603A1

; GENERAL INFORMATION:

; APPLICANT: Jonathon Henry ELLIS

; APPLICANT: Paul Andrew HAMBLEN

; APPLICANT: Paul Alexander WILSON

; APPLICANT: Alan Peter LEWIS

; TITLE OF INVENTION: IMMUNOGLOBULINS

; FILE REFERENCE: PB60608-2

; CURRENT APPLICATION NUMBER: US/11/177,648

; CURRENT FILING DATE: 2005-07-06

; PRIOR APPLICATION NUMBER: PCT/GB2004/005325

; PRIOR FILING DATE: 2004-12-20

; PRIOR APPLICATION NUMBER: GB0329711.6

; PRIOR FILING DATE: 2003-12-22

; PRIOR APPLICATION NUMBER: GB0329684.5

; PRIOR FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 113

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 94

; LENGTH: 462

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: 2A10 heavy chain humanised construct H21

US-11-177-648-94

Query Match 86.6%; Score 1624; DB 7; Length 462;

Best Local Similarity 68.8%; Pred. No. 1e-96;

Matches 319; Conservative 10; Mismatches 23; Indels 112; Gaps 2;

QY 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWHVKQNP 60

DB 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTSYMHHVWRQP 60

QY 61 GQLEWIGVSPGNDPFKNRFGKATLTADTSASTAYVELSLRSEDVAVYFCTRSN 120

DB 61 GQLEWIGVSPGNDPFKNRFGKATLTADTSASTAYVELSLRSEDVAVYFCTRSN 120

QY 121 MAYWGQGLTVVSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGAL 180

DB 119 QGWGQGLTVVSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGAL 178

QY 181 TSGVHTFPFPAVLQSSGLYSLSVVTPSSSLGTQYICNVNHPKSNKTKVDKKVPEPKSCDKT 240

DB 179 TSGVHTFPFPAVLQSSGLYSLSVVTPSSSLGTQYICNVNHPKSNKTKVDKKVPEPKSCDKT 238

QY 241 HTCPPCP----- 247

DB 239 HTCPPCPAPELAGAPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298

QY 248 -----GQP 250

DB 299 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 358

QY 251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSDGS 310

DB 359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSDGS 418

QY 311 FFYLSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354

DB 419 FFYLSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 462

RESULT 10

US-11-177-648-93

; Sequence 93, Application US/11177648

; Publication No. US20060029603A1

; GENERAL INFORMATION:

; APPLICANT: Jonathon Henry ELLIS

; APPLICANT: Paul Andrew HAMBLEN

; APPLICANT: Paul Alexander WILSON

; APPLICANT: Alan Peter LEWIS

; TITLE OF INVENTION: IMMUNOGLOBULINS

; FILE REFERENCE: PB60608-2

; CURRENT APPLICATION NUMBER: US/11/177,648

; CURRENT FILING DATE: 2005-07-06

; PRIOR APPLICATION NUMBER: PCT/GB2004/005325

; PRIOR FILING DATE: 2004-12-20

; PRIOR APPLICATION NUMBER: GB0329711.6

; PRIOR FILING DATE: 2003-12-22

; PRIOR APPLICATION NUMBER: GB0329684.5

; PRIOR FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 113

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 93

; LENGTH: 462

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: 2A10 heavy chain humanised construct H20

US-11-177-648-93

Query Match 86.5%; Score 1622; DB 7; Length 462;

Best Local Similarity 68.8%; Pred. No. 1.4e-96;

Matches 319; Conservative 10; Mismatches 23; Indels 112; Gaps 2;

QY 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWHVKQNP 60

DB 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTSYMHHVWRQP 60

QY 61 GQLEWIGVSPGNDPFKNRFGKATLTADTSASTAYVELSLRSEDVAVYFCTRSN 120

```
Db      61  GCGLEWIGNINPNSGGTNNFKSKATWTRDTSTSTAYMELSSLRSEDATVYC--ELG 118
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      121  MAYWGGTLLTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKOYFPEPPTVSMNSGAL 180
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      119  QGYWGGTLLTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 178
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      181  TSGVHTFPAVLQSSGLYSLSSVVTVSPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKT 240
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      179  TSGVHTFPAVLQSSGLYSLSSVVTVSPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKT 238
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      241  HTCPPCP----- 247
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      239  HTPCPCPAPELAGAPSVFLPPPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      248  -----GQP 250
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      299  VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 358
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      251  REPQVYTLPPSRDELTKNOVSLTCLVKGYFSPYSDIAVEWESNGQPENNYKTTPPVLDSDGS 310
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      359  REPQVYTLPPSRDELTKNOVSLTCLVKGYFSPYSDIAVEWESNGQPENNYKTTPPVLDSDGS 418
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      311  FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKLSLSLSPGK 354
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      419  FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKLSLSLSPGK 462
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
```

```
RESULT 11
US-11-177-648-92
; Sequence 92, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; PRIOR FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR FILING DATE: 2003-12-22
; PRIOR FILING DATE: 2003-12-22
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H19
US-11-177-648-92
```

```
Query Match      86.4%; Score 1621; DB 7; Length 462;
Best Local Similarity 68.5%; Pred. No. 1.6e-96;
Matches 318; Conservative 11; Mismatches 23; Indels 112; Gaps 2;

Qy      1  MGWSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNP 60
Db      1  MGWSLILLFLVATATGVHSQVQLVQSGAEVVKPGASVKISKASGYTFTSYNWHWVRQP 60
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      61  GORLEWIGYFSPGNDDFKYNRERFKGKATLTADTSASTAYVELSLRSEDATVYFCTRSLN 120
Db      61  GCGLEWIGNINPNSGGTNNFKSKATWTRDTSTSTAYMELSSLRSEDATVYC--ELG 118
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      121  MAYWGGTLLTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 180
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      119  QGYWGGTLLTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 178
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
```

```
Qy      181  TSGVHTFPAVLQSSGLYSLSSVVTVSPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKT 240
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      179  TSGVHTFPAVLQSSGLYSLSSVVTVSPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKT 238
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      241  HTCPPCP----- 247
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      239  HTPCPCPAPELAGAPSVFLPPPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      248  -----GQP 250
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      299  VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 358
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      251  REPQVYTLPPSRDELTKNOVSLTCLVKGYFSPYSDIAVEWESNGQPENNYKTTPPVLDSDGS 310
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      359  REPQVYTLPPSRDELTKNOVSLTCLVKGYFSPYSDIAVEWESNGQPENNYKTTPPVLDSDGS 418
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      311  FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKLSLSLSPGK 354
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      419  FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKLSLSLSPGK 462
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|

RESULT 12
US-11-177-648-27
; Sequence 27, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; PRIOR FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H6
US-11-177-648-27
```

```
Query Match      86.3%; Score 1619; DB 7; Length 462;
Best Local Similarity 68.5%; Pred. No. 2.2e-96;
Matches 318; Conservative 11; Mismatches 23; Indels 112; Gaps 2;

Qy      1  MGWSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNP 60
Db      1  MGWSLILLFLVATATGVHSQVQLVQSGAEVVKPGASVKISKASGYTFTSYNWHWVRQP 60
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      61  GORLEWIGYFSPGNDDFKYNRERFKGKATLTADTSASTAYVELSLRSEDATVYFCTRSLN 120
Db      61  GCGLEWIGNINPNSGGTNNFKSKATWTRDTSTSTAYMELSSLRSEDATVYC--ELG 118
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      121  MAYWGGTLLTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 180
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      119  QGYWGGTLLTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 178
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      181  TSGVHTFPAVLQSSGLYSLSSVVTVSPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKT 240
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      179  TSGVHTFPAVLQSSGLYSLSSVVTVSPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKT 238
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      241  HTCPPCP----- 247
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      239  HTPCPCPAPELAGAPSVFLPPPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
```

```

QY      248 -----GQP 250
Db      299 VHNAKTKPREEQNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIETKISKAKGQP 358
QY      251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPVLDSGDS 310
Db      359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPVLDSGDS 418
QY      311 FFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYTQKLSLSLSPGK 354
Db      419 FFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYTQKLSLSLSPGK 462

RESULT 13
US-11-177-648-28
; Sequence 28, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; PRIOR FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H700
US-11-177-648-28

Query Match      86.1%; Score 1616; DB 7; Length 462;
Best Local Similarity 68.5%; Pred. No. 3.3e-96;
Matches 318; Conservative 10; Mismatches 24; Indels 112; Gaps 2;

QY      1  MGSLLILFLVAVATRVLSQVLQVSGAEVVKPGASVKISKCKASGYTFTDTHAIHWKQP 60
Db      1  MGSCLILFLVATATGVHSGVQLVQSGAEVVKPGASVKISCKASGYTFTSYMHWRQAP 60
QY      61  GORLEWIGVSPGNDPFKYNRPKGKATLTADTSASTAYVELSLRSEDYAVYFCTRSLN 120
Db      61  GQGLEWIGNINSPNGTNYNEKFKSRVTWTRDTSTSTAYMELSLRSEDYAVYFCTRSLN 118
QY      121  MAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 180
Db      119  QGYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 178
QY      181  TSGVHTFPFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT 240
Db      179  TSGVHTFPFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT 238
QY      241  HTCCPPCP----- 247
Db      239  HTCCPPCPAPELAGAPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298
QY      248 -----GQP 250
Db      299 VHNAKTKPREEQNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIETKISKAKGQP 358
QY      251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPVLDSGDS 310

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Db      359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPVLDSGDS 418
QY      311 FFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYTQKLSLSLSPGK 354
Db      419 FFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYTQKLSLSLSPGK 462

RESULT 14
US-11-177-648-98
; Sequence 98, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; PRIOR FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H25
US-11-177-648-98

Query Match      86.0%; Score 1614; DB 7; Length 462;
Best Local Similarity 68.1%; Pred. No. 4.5e-96;
Matches 316; Conservative 12; Mismatches 24; Indels 112; Gaps 2;

QY      1  MGSLLILFLVAVATRVLSQVLQVSGAEVVKPGASVKISKCKASGYTFTDTHAIHWKQP 60
Db      1  MGSCLILFLVATATGVHSGVQLVQSGAEVVKPGASVKISCKASGYTFTSYMHWRQRP 60
QY      61  GORLEWIGVSPGNDPFKYNRPKGKATLTADTSASTAYVELSLRSEDYAVYFCTRSLN 120
Db      61  GQGLEWIGNINSPNGTNYNEKFKSRVTWTRDTSTSTAYMELSLRSEDYAVYFCTRSLN 118
QY      121  MAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 180
Db      119  QGYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 178
QY      181  TSGVHTFPFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT 240
Db      179  TSGVHTFPFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT 238
QY      241  HTCCPPCP----- 247
Db      239  HTCCPPCPAPELAGAPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298
QY      248 -----GQP 250
Db      299 VHNAKTKPREEQNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIETKISKAKGQP 358
QY      251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPVLDSGDS 310
Db      359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPVLDSGDS 418
QY      311 FFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYTQKLSLSLSPGK 354
Db      419 FFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYTQKLSLSLSPGK 462

```

RESULT 15

US-11-177-648-26  
; Sequence 26, Application US/11177648  
; Publication No. US20060029603A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonathon Henry ELLIS  
; APPLICANT: Paul Andrew HAMBLIN  
; APPLICANT: Paul Alexander WILSON  
; APPLICANT: Alan Peter LEWIS  
; TITLE OF INVENTION: IMMUNOGLOBULINS  
; FILE REFERENCE: PB60608-2  
; CURRENT APPLICATION NUMBER: US/11/177,648  
; CURRENT FILING DATE: 2005-07-06  
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325  
; PRIOR FILING DATE: 2004-12-20  
; PRIOR APPLICATION NUMBER: GB0329711.6  
; PRIOR FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: GB0329684.5  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 2A10 heavy chain humanised construct H5  
US-11-177-648-26

Query Match 85.9%; Score 1612; DB 7; Length 462;  
Best Local Similarity 68.1%; Pred No. 6e-96;  
Matches 316; Conservative 12; Mismatches 24; Indels 112; Gaps 2;  
  
QY 1 MGWSILFLVAVATRVLSQVLQVSGAEVWVKPGASVKISKASGYTFDTHAIHWKQNP 60  
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
1 MGWSCILFLVATATGVHSQVLQVSGAEVWVKPGASVKISKASGYTFDTHAIHWKQNP 60  
QY 61 GORLEWIGVFGPNDGDFKNERPKAKILTADTSATAYVELSSLRSEDTAVYFCTRSIN 120  
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
61 GQGLEWGMGNINPNSGNTNNEKFKSRVTMDTSTSTAYMELSSLRSEDTAVYYC--ELG 118  
QY 121 MAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGAL 180  
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
119 QGYWCGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGAL 178  
QY 181 TSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTVICNVNHRKPSNTKVDKVEPKSCDKT 240  
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
179 TSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTVICNVNHRKPSNTKVDKVEPKSCDKT 238  
QY 241 HTCPKCP----- 247  
Db :||||| :  
239 HTCPKCPAPELAGAPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298  
QY 248 -----GQP 250  
Db :||||| :  
299 VHNAKTKPREEQNYSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIEKTISKAKGQP 358  
QY 251 REPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGDS 310  
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
359 REPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGDS 418  
QY 311 PFLYSKLTVDKSRWQQGNVFCFVSNVHEALHNHYTQKSLSLSPGK 354  
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
419 PFLYSKLTVDKSRWQQGNVFCFVSNVHEALHNHYTQKSLSLSPGK 462

Search completed: February 16, 2006, 10:43:38  
Job time : 16.1111 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2006, 10:38:47 ; Search time 136.475 Seconds  
(without alignments)  
1083.802 Million cell updates/sec

Title: US-10-058-069-7  
Perfect score: 1876  
Sequence: 1 MGWSILLFLVAVATRVLSQ.....MHEALHNHYTKLSLSPOK 354

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*

- 1: /cgn2\_6/prodata1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/prodata1/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/prodata1/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/prodata1/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/prodata1/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/prodata1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1770	94.3	347	5	US-10-880-028-18
2	1770	94.3	347	5	US-10-880-320-18
3	1763.5	94.0	360	5	US-10-880-028-22
4	1763.5	94.0	360	5	US-10-880-320-22
5	1762.5	93.9	362	5	US-10-880-028-23
6	1762.5	93.9	362	5	US-10-880-320-23
7	1755.5	93.6	362	5	US-10-880-028-26
8	1755.5	93.6	362	5	US-10-880-320-26
9	1613.5	86.0	731	3	US-09-825-012-46
10	1613.5	86.0	741	3	US-09-825-012-55
11	1613	86.0	470	6	US-11-019-180-4
12	1608.5	85.7	729	3	US-09-825-012-52
13	1608.5	85.7	739	3	US-09-825-012-61
14	1603	85.4	470	4	US-10-216-484-89
15	1603	85.4	470	4	US-10-384-933-89
16	1602.5	85.4	730	3	US-09-825-012-49
17	1602.5	85.4	740	3	US-09-825-012-58
18	1595	85.0	470	4	US-10-216-484-143
19	1595	85.0	470	4	US-10-384-933-143
20	1593	84.9	470	4	US-10-216-484-145
21	1593	84.9	470	4	US-10-384-933-145
22	1592	84.9	470	4	US-10-216-484-117
23	1592	84.9	470	4	US-10-216-484-147
24	1592	84.9	470	4	US-10-384-933-117
25	1592	84.9	470	4	US-10-384-933-147
26	1579	84.2	468	5	US-10-981-738-13
27	1579	84.2	470	4	US-10-216-484-157

ALIGNMENTS

RESULT 1  
US-10-880-028-18  
; Sequence 18, Application US/10880028  
; Publication No. US20050163782A1  
; GENERAL INFORMATION:  
; APPLICANT: BRASLAWSKY, Gary R.  
; APPLICANT: GLASER, Scott  
; APPLICANT: YANG, Tzung-Hong  
; APPLICANT: HOPP, Jennifer  
; APPLICANT: CHINN, Paul  
; TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS  
; TITLE OF INVENTION: OF BINDING POLYPEPTIDES  
; FILE REFERENCE: IDV-001  
; CURRENT APPLICATION NUMBER: US/10/880,028  
; CURRENT FILING DATE: 2004-06-28  
; PRIOR APPLICATION NUMBER: 60/483877  
; PRIOR FILING DATE: 2003-06-27  
; PRIOR APPLICATION NUMBER: 60/508810  
; PRIOR FILING DATE: 2003-10-03  
; PRIOR APPLICATION NUMBER: 60/515351  
; PRIOR FILING DATE: 2003-10-28  
; PRIOR APPLICATION NUMBER: 60/516030  
; PRIOR FILING DATE: 2003-10-30  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 347  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-880-028-18

Query Match 94.3%; Score 1770; DB 5; Length 347;  
Best Local Similarity 96.5%; Pred. No. 1-7e-112;  
Matches 335; Conservative 0; Mismatches 0; Indels 12; Gaps 1;  
QY 20 QVQLVQSGAEVVPKASVKISKASGYTPTDTHAIHWKONPGORLEWIGYFSPGNDFFKY 79  
Db 1 QVQLVQSGAEVVPKASVKISKASGYTPTDTHAIHWKONPGORLEWIGYFSPGNDFFKY 60  
QY 80 NERFVGKATLTADTASNTAYVELSLRSEDVAVFCTRLSNWAYWGQGLVTVSSASTKG 139  
Db 61 NERFVGKATLTADTASNTAYVELSLRSEDVAVFCTRLSNWAYWGQGLVTVSSASTKG 120  
QY 140 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSL 199  
Db 121 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSL 180  
QY 200 SSVVTVPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPPCP----- 247

Sequence 157, Appl  
Sequence 5, Appl  
Sequence 12, Appl  
Sequence 40, Appl  
Sequence 40, Appl  
Sequence 44, Appl  
Sequence 46, Appl  
Sequence 44, Appl  
Sequence 44, Appl  
Sequence 47, Appl  
Sequence 47, Appl  
Sequence 47, Appl  
Sequence 53, Appl  
Sequence 59, Appl  
Sequence 41, Appl



;/ TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS  
;/ FILE REFERENCE: IDV-001  
;/ CURRENT FILING DATE: 2004-06-28  
;/ CURRENT APPLICATION NUMBER: US/10/880,320  
;/ PRIOR FILING DATE: 2004-06-27  
;/ PRIOR FILING DATE: 2003-06-27  
;/ PRIOR FILING DATE: 2003-06-27  
;/ PRIOR FILING DATE: 2003-06-27  
;/ PRIOR FILING DATE: 2003-10-03  
;/ PRIOR FILING DATE: 2003-10-03  
;/ PRIOR FILING DATE: 2003-10-03  
;/ PRIOR FILING DATE: 2003-10-03  
;/ PRIOR FILING DATE: 2003-10-03  
;/ NUMBER OF SEQ ID NOS: 53  
;/ SOFTWARE: FastSeq for Windows Version 4.0  
;/ SEQ ID NO 22  
;/ LENGTH: 360  
;/ TYPE: PRT  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ OTHER INFORMATION: Synthetic construct  
US-10-880-320-22

Query Match 94.0%; Score 1763.5; DB 5; Length 360;  
Best Local Similarity 93.1%; Pred. No. 4.9e-112;  
Matches 335; Conservative 0; Mismatches 0; Indels 25; Gaps 1;  
  
QY 20 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHWKQNPQORLEWIGYFSPGNDDFKY 79  
DB 1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHWKQNPQORLEWIGYFSPGNDDFKY 60  
  
QY 80 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRSINMAYWQGTLLTVSSASTKG 139  
DB 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRSINMAYWQGTLLTVSSASTKG 120  
  
QY 140 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL 199  
DB 121 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL 180  
  
QY 200 SSVVTVPSSSLGTQTYICNVNHPKSNTKVDKKEPKSCDKTHTCTPCP----- 247  
DB 181 SSVVTVPSSSLGTQTYICNVNHPKSNTKVDKKEPKSCDKTHTCTPCPCKDTPPPCP 240  
  
QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 294  
DB 241 RCPGGSGGGSGGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 300  
  
QY 295 ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354  
DB 301 ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 360

RESULT 5  
US-10-880-028-23  
;/ Sequence 23, Application US/10880028  
;/ Publication No. US20050163782A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: BRASLAWSKY, Gary R.  
;/ APPLICANT: GLASER, Scott  
;/ APPLICANT: YANG, Tzung-Hong  
;/ APPLICANT: HOPP, Jennifer  
;/ APPLICANT: CHINN, Paul  
;/ TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS  
;/ TITLE OF INVENTION: OF BINDING POLYPEPTIDES  
;/ FILE REFERENCE: IDV-001  
;/ CURRENT APPLICATION NUMBER: US/10/880,028  
;/ CURRENT FILING DATE: 2004-06-28  
;/ PRIOR APPLICATION NUMBER: 60/483877  
;/ PRIOR FILING DATE: 2003-06-27  
;/ PRIOR APPLICATION NUMBER: 60/508810  
;/ PRIOR FILING DATE: 2003-10-03  
;/ PRIOR APPLICATION NUMBER: 60/515351  
;/ PRIOR FILING DATE: 2003-10-28

;/ PRIOR APPLICATION NUMBER: 60/516030  
;/ PRIOR FILING DATE: 2003-10-30  
;/ NUMBER OF SEQ ID NOS: 53  
;/ SOFTWARE: FastSeq for Windows Version 4.0  
;/ SEQ ID NO 23  
;/ LENGTH: 362  
;/ TYPE: PRT  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ OTHER INFORMATION: Synthetic construct  
US-10-880-028-23

Query Match 93.9%; Score 1762.5; DB 5; Length 362;  
Best Local Similarity 92.5%; Pred. No. 5.8e-112;  
Matches 335; Conservative 0; Mismatches 0; Indels 27; Gaps 1;  
  
QY 20 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHWKQNPQORLEWIGYFSPGNDDFKY 79  
DB 1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHWKQNPQORLEWIGYFSPGNDDFKY 60  
  
QY 80 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRSINMAYWQGTLLTVSSASTKG 139  
DB 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRSINMAYWQGTLLTVSSASTKG 120  
  
QY 140 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL 199  
DB 121 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL 180  
  
QY 200 SSVVTVPSSSLGTQTYICNVNHPKSNTKVDKKEPKSCDKTHTCTPCP----- 247  
DB 181 SSVVTVPSSSLGTQTYICNVNHPKSNTKVDKKEPKSCDKTHTCTPCPCKDTPPPCP 240  
  
QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 292  
DB 241 RCPAPGGSGGGSGGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 300  
  
QY 293 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP 352  
DB 301 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP 360  
  
QY 353 GK 354  
DB 361 GK 362

RESULT 6  
US-10-880-320-23  
;/ Sequence 23, Application US/10880320  
;/ Publication No. US20050163783A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: BRASLAWSKY, Gary R.  
;/ APPLICANT: GLASER, Scott  
;/ APPLICANT: YANG, Tzung-Hong  
;/ APPLICANT: HOPP, Jennifer  
;/ APPLICANT: CHINN, Paul  
;/ TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS  
;/ TITLE OF INVENTION: OF BINDING POLYPEPTIDES  
;/ FILE REFERENCE: IDV-001  
;/ CURRENT APPLICATION NUMBER: US/10/880,320  
;/ CURRENT FILING DATE: 2004-06-28  
;/ PRIOR APPLICATION NUMBER: 60/483877  
;/ PRIOR FILING DATE: 2003-06-27  
;/ PRIOR APPLICATION NUMBER: 60/508810  
;/ PRIOR FILING DATE: 2003-10-03  
;/ PRIOR APPLICATION NUMBER: 60/515351  
;/ PRIOR FILING DATE: 2003-10-28  
;/ PRIOR APPLICATION NUMBER: 60/516030  
;/ PRIOR FILING DATE: 2003-10-30  
;/ NUMBER OF SEQ ID NOS: 53  
;/ SOFTWARE: FastSeq for Windows Version 4.0  
;/ SEQ ID NO 23  
;/ LENGTH: 362  
;/ TYPE: PRT



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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-880-320-23

Query Match      93.9%; Score 1762.5; DB 5; Length 362;
Best Local Similarity 92.5%; Pred. No. 5.8e-112;
Matches 335; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

QY 20 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAIIHWVKQNPQORLEWIGYFSPGNDDFKY 79
DB 1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAIIHWVKQNPQORLEWIGYFSPGNDDFKY 60

QY 80 NERFKGKATLTADTSASTAYVELSLRSEDTAIFYCTRSLNMYWGQGLTVTVSSASTKG 139
DB 61 NERFKGKATLTADTSASTAYVELSLRSEDTAIFYCTRSLNMYWGQGLTVTVSSASTKG 120

QY 140 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL 199
DB 121 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL 180

QY 200 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPPCP----- 247
DB 181 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPPCP----- 240

QY 248 -----GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 292
DB 241 RCPAPGGSGGGSGGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 300

QY 293 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP 352
DB 301 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP 360

QY 353 GK 354
DB 361 GK 362

RESULT 7
US-10-880-028-26
; Sequence 26, Application US/10880028
; Publication No. US20050163782A1
; GENERAL INFORMATION:
; APPLICANT: BRASLAWSKY, Gary R.
; APPLICANT: GLASER, Scott
; APPLICANT: YANG, Tzung-Horng
; APPLICANT: HOPP, Jennifer
; APPLICANT: CHINN, Paul
; TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS
; FILE REFERENCE: IDV-001
; CURRENT APPLICATION NUMBER: US/10/880,028
; CURRENT FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: 60/483877
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/508810
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/515351
; PRIOR FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: 60/516030
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-880-028-26

Query Match      93.6%; Score 1755.5; DB 5; Length 362;
Best Local Similarity 92.0%; Pred. No. 1.7e-111;
Matches 333; Conservative 1; Mismatches 1; Indels 27; Gaps 1;

QY 20 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAIIHWVKQNPQORLEWIGYFSPGNDDFKY 79
DB 1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAIIHWVKQNPQORLEWIGYFSPGNDDFKY 60

QY 80 NERFKGKATLTADTSASTAYVELSLRSEDTAIFYCTRSLNMYWGQGLTVTVSSASTKG 139
DB 61 NERFKGKATLTADTSASTAYVELSLRSEDTAIFYCTRSLNMYWGQGLTVTVSSASTKG 120

QY 140 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL 199
DB 121 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL 180

QY 200 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPPCP----- 247
DB 181 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPPCP----- 240

QY 248 -----GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 292
DB 241 RCPAPGGSGGGSGGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 300

QY 293 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP 352
DB 301 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP 360

QY 353 GK 354
DB 361 GK 362
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-880-320-23

Query Match      93.9%; Score 1762.5; DB 5; Length 362;
Best Local Similarity 92.5%; Pred. No. 5.8e-112;
Matches 335; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

QY 20 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAIIHWVKQNPQORLEWIGYFSPGNDDFKY 79
DB 1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAIIHWVKQNPQORLEWIGYFSPGNDDFKY 60

QY 80 NERFKGKATLTADTSASTAYVELSLRSEDTAIFYCTRSLNMYWGQGLTVTVSSASTKG 139
DB 61 NERFKGKATLTADTSASTAYVELSLRSEDTAIFYCTRSLNMYWGQGLTVTVSSASTKG 120

QY 140 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL 199
DB 121 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL 180

QY 200 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPPCP----- 247
DB 181 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPPCP----- 240

QY 248 -----GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 292
DB 241 RCPAPGGSGGGSGGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 300

QY 293 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP 352
DB 301 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP 360

QY 353 GK 354
DB 361 GK 362

RESULT 8
US-10-880-320-26
; Sequence 26, Application US/10880320
; Publication No. US20050163783A1
; GENERAL INFORMATION:
; APPLICANT: BRASLAWSKY, Gary R.
; APPLICANT: GLASER, Scott
; APPLICANT: YANG, Tzung-Horng
; APPLICANT: HOPP, Jennifer
; APPLICANT: CHINN, Paul
; TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS
; FILE REFERENCE: IDV-001
; CURRENT APPLICATION NUMBER: US/10/880,320
; CURRENT FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: 60/483877
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/508810
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/515351
; PRIOR FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: 60/516030
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-880-320-26

Query Match      93.6%; Score 1755.5; DB 5; Length 362;
Best Local Similarity 92.0%; Pred. No. 1.7e-111;
Matches 333; Conservative 1; Mismatches 1; Indels 27; Gaps 1;

QY 20 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAIIHWVKQNPQORLEWIGYFSPGNDDFKY 79
DB 1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAIIHWVKQNPQORLEWIGYFSPGNDDFKY 60

QY 80 NERFKGKATLTADTSASTAYVELSLRSEDTAIFYCTRSLNMYWGQGLTVTVSSASTKG 139
DB 61 NERFKGKATLTADTSASTAYVELSLRSEDTAIFYCTRSLNMYWGQGLTVTVSSASTKG 120

QY 140 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL 199
DB 121 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL 180

QY 200 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPPCP----- 247
DB 181 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPPCP----- 240

QY 248 -----GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 292
DB 241 RCPAPGGSGGGSGGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 300

QY 293 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP 352
DB 301 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP 360

QY 353 GK 354
DB 361 GK 362
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Db 61 NERFKGAYITADTSASTAYVELSLRSEDATVYFCARLNMAYMGQGLTVTVSSASTKG 120
Qy 140 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNNSGALTSGVHTFPAVLQSSGLYSL 199
Db 121 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNNSGALTSGVHTFPAVLQSSGLYSL 180
Qy 200 SSVVTVPSSSLGQTQYICNNVHSPNTKVDKVEPKSCDKTHTCPPCP 247
Db 181 SSVVTVPSSSLGQTQYICNNVHSPNTKVDKVEPKSCDKTHTCPPCPKSCDTTPPCP 240
Qy 248 -----COPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNG 292
Db 241 RCPAPGGSGGGGQOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNG 300
Qy 293 QPENNYKTPPVLDSGGSFFLYSLKLVDSRWQOGNVFSCSVNHEALHNNHYTKSLSLSP 352
Db 301 QPENNYKTPPVLDSGGSFFLYSLKLVDSRWQOGNVFSCSVNHEALHNNHYTKSLSLSP 360
Qy 353 GK 354
Db 361 GK 362

RESULT 9
US-09-825-012-46
; Sequence 46, Application US/09825012
; Patent No. US2002012798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFg1 heavy chain - DNase I fusion
US-09-825-012-46

Query Match 86.0%; Score 1613.5; DB 3; Length 731;
Best Local Similarity 67.7%; Pred. No. 1.8e-101;
Matches 316; Conservative 18; Mismatches 20; Indels 113; Gaps 2;

Qy 1 MGWLLILFLVAVATRVLSQVOLVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60
Db 1 MGWSCIILFLVATATGVHSQVOLVSGAEVVKPGASVKISCKASGYTFSAIEWVRQAP 60
Qy 61 GORLEWIGYFSPGNDDFKYNRFKGRVTVTRDTSTNTAYMELSSLRSEDATVYFCRSLN 120
Db 61 GKGLEWVGILPGSNNSRNYEKFKGRVTVTRDTSTNTAYMELSSLRSEDATVYFCARSYD 120
Qy 121 ---MAYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSN 177
Db 121 FAWFAYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSN 180
Qy 178 GALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNNVHSPNTKVDKVEPKSC 237
Db 181 GALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNNVHSPNTKVDKVEPKSC 240
Qy 238 DKTHTCPPCP----- 247
Db 241 DKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 300
Qy 248 ----- 247
Db 301 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDLNMGKEYCKVSNKALPAPIEKTISKAK 360
Qy 248 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDS 307
Db 361 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDS 420
Qy 308 DGSFFLYSKLTVDSRWQOGNVFSCSVNHEALHNNHYTKSLSLSPGK 354
Db 421 DGSFFLYSKLTVDSRWQOGNVFSCSVNHEALHNNHYTKSLSLSPGK 467
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Db 301 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDLNMGKEYCKVSNKALPAPIEKTISKAK 360
Qy 248 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDS 307
Db 361 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDS 420
Qy 308 DGSFFLYSKLTVDSRWQOGNVFSCSVNHEALHNNHYTKSLSLSPGK 354
Db 421 DGSFFLYSKLTVDSRWQOGNVFSCSVNHEALHNNHYTKSLSLSPGK 467

RESULT 10
US-09-825-012-55
; Sequence 55, Application US/09825012
; Patent No. US2002012798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 741
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFg1 heavy chain - DNase I fusion
US-09-825-012-55

Query Match 86.0%; Score 1613.5; DB 3; Length 741;
Best Local Similarity 67.7%; Pred. No. 1.8e-101;
Matches 316; Conservative 18; Mismatches 20; Indels 113; Gaps 2;

Qy 1 MGWLLILFLVAVATRVLSQVOLVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60
Db 1 MGWSCIILFLVATATGVHSQVOLVSGAEVVKPGASVKISCKASGYTFSAIEWVRQAP 60
Qy 61 GORLEWIGYFSPGNDDFKYNRFKGRVTVTRDTSTNTAYMELSSLRSEDATVYFCRSLN 120
Db 61 GKGLEWVGILPGSNNSRNYEKFKGRVTVTRDTSTNTAYMELSSLRSEDATVYFCARSYD 120
Qy 121 ---MAYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSN 177
Db 121 FAWFAYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSN 180
Qy 178 GALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNNVHSPNTKVDKVEPKSC 237
Db 181 GALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNNVHSPNTKVDKVEPKSC 240
Qy 238 DKTHTCPPCP----- 247
Db 241 DKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 300
Qy 248 ----- 247
Db 301 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDLNMGKEYCKVSNKALPAPIEKTISKAK 360
Qy 248 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDS 307
Db 361 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDS 420
Qy 308 DGSFFLYSKLTVDSRWQOGNVFSCSVNHEALHNNHYTKSLSLSPGK 354
Db 421 DGSFFLYSKLTVDSRWQOGNVFSCSVNHEALHNNHYTKSLSLSPGK 467
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RESULT 11
US-11-019-180-4
; Sequence 4, Application US/11019180
; Publication No. US20050158828A1
; GENERAL INFORMATION:
; APPLICANT: BRASLAWSKY, GARY R.
; APPLICANT: HANNA, NABIL
; APPLICANT: HARIHARAN, KANDASAMY
; APPLICANT: LABARRE, MICHAEL J.
; APPLICANT: HUYNH, TRI B.
; TITLE OF INVENTION: PRODUCTION OF TETRAVALENT ANTIBODIES
; FILE REFERENCE: 23522.0584
; CURRENT APPLICATION NUMBER: US/11/019,180
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US/09/238,741
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: "Dimeric" Anti-CD20 Heavy Chain (Version 1)
US-11-019-180-4

Query Match      86.0%; Score 1613; DB 6; Length 470;
Best Local Similarity 67.7%; Pred. No. 1.2e-101;
Matches 318; Conservative 13; Mismatches 23; Indels 116; Gaps 2;

QY      1  MGWSLILLFLVAVATRVLSQVLVQSGAEVVKPGASVKISKASGVTFTDHAHVMKQNP 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1  MGWSLILLFLVAVATRVLSQVLVQSGAEVVKPGASVKISKASGVTFTSYNHWKQTP 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61  GORLEWIGVSPGNDDFKYNRFKGGKATLTADTSASTAYVELSSLRSEDTAVYFCTRSLN 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  GRGLEWIGVSPGNDDFKYNRFKGGKATLTADTSASTAYVELSSLRSEDTAVYFCTRSLN 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61  GRGLEWIGVSPGNDDFKYNRFKGGKATLTADTSASTAYVELSSLRSEDTAVYFCTRSLN 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  GRGLEWIGVSPGNDDFKYNRFKGGKATLTADTSASTAYVELSSLRSEDTAVYFCTRSLN 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      121  MA-----YWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVVS 174
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121  YGDMWYFNVWGAGTTVTVSSAASKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVVS 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      175  WNSGALTSQVHTFPFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEP 234
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181  WNSGALTSQVHTFPFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEP 240
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      235  KSCDKTHTCPPCP----- 247
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241  KSCDKTHTCPPCPAPPELLGGPSVFLPAPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      248  ----- 247
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301  YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      248  ----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 304
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      361  KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      305  LPSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 354
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      421  LPSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLCPGK 470
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-09-825-012-52
; Sequence 52, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
```

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; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFGL heavy chain - DNase I fusion
US-09-825-012-52

Query Match      85.7%; Score 1608.5; DB 3; Length 729;
Best Local Similarity 67.6%; Pred. No. 3.9e-101;
Matches 315; Conservative 18; Mismatches 20; Indels 113; Gaps 2;

QY      1  MGWSLILLFLVAVATRVLSQVLVQSGAEVVKPGASVKISKASGVTFTDHAHVMKQNP 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1  MGWSLILLFLVAVATRVLSQVLVQSGAEVVKPGASVKISKASGVTFTSYNHWKQNP 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61  GORLEWIGVSPGNDDFKYNRFKGGKATLTADTSASTAYVELSSLRSEDTAVYFCTRSLN 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  GRGLEWIGVSPGNDDFKYNRFKGGKATLTADTSASTAYVELSSLRSEDTAVYFCTRSLN 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      121  ---MAYWQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVVS 177
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121  FAWFAYWQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVVS 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      178  GALTSGVHTFPFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSC 237
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181  GALTSGVHTFPFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSC 240
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      238  DKHTHTCPPCP----- 247
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241  DKHTHTCPPCPAPPELLGGPSVFLPAPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 300
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      248  ----- 247
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301  GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 360
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      248  GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 307
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      361  GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 420
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      308  DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPG 353
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      421  DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPG 466
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-09-825-012-61
; Sequence 61, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Humanised HMF61 heavy chain - DNase I fusion  
US-09-825-012-61

```
Query Match      85.7%; Score 1608.5; DB 3; Length 739;
Best Local Similarity 67.6%; Pred. No. 3.9e-101;
Matches 315; Conservative 18; Mismatches 20; Indels 113; Gaps 2;

QY 1 MGWSSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60
DB 1 MGWSSLILFLVATATGVSQVQLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60

QY 61 GQRLWIGYFSPGNDDFKYNRFKPKATLTADTSASTAYVELSSLRSEDATVYFCTRSLN 120
DB 61 GQRLWIGYFSPGNDDFKYNRFKPKATLTADTSASTAYVELSSLRSEDATVYFCTRSLN 120

QY 61 GQRLWIGYFSPGNDDFKYNRFKPKATLTADTSASTAYVELSSLRSEDATVYFCTRSLN 120
DB 61 GQRLWIGYFSPGNDDFKYNRFKPKATLTADTSASTAYVELSSLRSEDATVYFCTRSLN 120

QY 121 MA-----YWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYPPEPTVVS 174
DB 121 YSNWYFDVWGEGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYPPEPTVVS 180

QY 175 WNSGALTSGVHFPFPAVLQSSGLYSLSVVTVPSSTLGTQTYICNVNHHKPSNTKVDKVEP 234
DB 181 WNSGALTSGVHFPFPAVLQSSGLYSLSVVTVPSSTLGTQTYICNVNHHKPSNTKVDKVEP 240

QY 235 KSCDKTHTCPPCP----- 247
DB 241 KSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300

QY 248 ----- 247
DB 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360

QY 248 ----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 304
DB 361 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420

QY 305 LQSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 354
DB 421 LQSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 470

RESULT 14
US-10-216-484-89
; Sequence 89, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT FILING DATE: 2000-02-09
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 89
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-89

Query Match      85.4%; Score 1603; DB 4; Length 470;
Best Local Similarity 67.0%; Pred. No. 5.6e-101;
Matches 315; Conservative 17; Mismatches 22; Indels 116; Gaps 2;

QY 1 MGWSSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60
DB 1 MGWSSLILFLVATATGVSQVQLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60

QY 61 GQRLWIGYFSPGNDDFKYNRFKPKATLTADTSASTAYVELSSLRSEDATVYFCTRSLN 120
DB 61 GQRLWIGYFSPGNDDFKYNRFKPKATLTADTSASTAYVELSSLRSEDATVYFCTRSLN 120

QY 121 MA-----YWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYPPEPTVVS 174
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US-10-384-933-89  
; Sequence 89, Application US/10384933  
; Publication No. US20030170817A1  
; GENERAL INFORMATION:  
; APPLICANT: Serizawa, No. US20030170817A1ufusa  
; APPLICANT: Haruyama, Hideyuki  
; APPLICANT: Nakahara, Kaori  
; APPLICANT: Tamaki, Ikuko  
; APPLICANT: Takahashi, Tohru  
; TITLE OF INVENTION: Anti-Fas Antibodies  
; FILE REFERENCE: 980126CIP/HG  
; CURRENT FILING DATE: 2003-02-05  
; PRIOR FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: US/09/499,662  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583  
; NUMBER OF SEQ ID NOS: 165  
; SEQ ID NO 89  
; LENGTH: 470  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy  
; OTHER INFORMATION: chain of humanized anti-Fas antibody  
US-10-384-933-89

Query Match 85.4%; Score 1603; DB 4; Length 470;  
Best Local Similarity 67.0%; Pred. No. 5.6e-101;  
Matches 315; Conservative 17; Mismatches 22; Indels 116; Gaps 2;

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QY 1 MGWSSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60
DB 1 MGWSSLILFLVATATGVSQVQLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60

QY 61 GQRLWIGYFSPGNDDFKYNRFKPKATLTADTSASTAYVELSSLRSEDATVYFCTRSLN 120
DB 61 GQRLWIGYFSPGNDDFKYNRFKPKATLTADTSASTAYVELSSLRSEDATVYFCTRSLN 120

QY 121 MA-----YWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYPPEPTVVS 174
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121 YNNMYFDVWGGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVVS 180
QY
175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVFPPSSSLGTQTYICNVNHKPSNTKVDKKVEP 234
Db
181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVFPPSSSLGTQTYICNVNHKPSNTKVDKKVEP 240
QY
235 KSCDKHTHTCPPCP----- 247
Db
241 KSCDKHTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
QY
248 ----- 247
Db
301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
QY
248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 304
Db
361 KAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
QY
305 LDSDSGFFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQKSLSLSPGK 354
Db
421 LDSDSGFFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQKSLSLSPGK 470
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Search completed: February 16, 2006, 10:43:10  
Job time : 138.475 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 16, 2006, 10:23:17 ; Search time 39.3333 Seconds  
(without alignments)  
744.081 Million cell updates/sec

Title: US-10-058-069-7  
Perfect score: 1876  
Sequence: 1 MGWSLFLFLVAVATRVLSQ.....MHEALHNHYTKSLSLSPGK 354

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5 COMB.pep.\*
- 2: /cgn2\_6/prodata/1/iaa/6 COMB.pep.\*
- 3: /cgn2\_6/prodata/1/iaa/H COMB.pep.\*
- 4: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*
- 5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*
- 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1613	86.0	470	2	US-09-238-741-4 Sequence 4, Appl
2	1559	83.1	466	2	US-09-698-705-11 Sequence 11, Appl
3	1549	82.6	472	2	US-09-301-593-43 Sequence 43, Appl
4	1541	82.1	449	1	US-08-458-516-13 Sequence 13, Appl
5	1524	81.2	472	2	US-09-301-593-30 Sequence 30, Appl
6	1509.5	80.5	489	2	US-10-104-047-3329 Sequence 3329, Ap
7	1506	80.3	476	1	US-08-378-939-10 Sequence 10, Appl
8	1501	80.0	468	2	US-09-485-737B-67 Sequence 67, Appl
9	1501	80.0	468	2	US-10-071-485-67 Sequence 67, Appl
10	1501	80.0	711	2	US-09-485-737B-90 Sequence 90, Appl
11	1495.5	79.7	467	2	US-10-071-485-90 Sequence 90, Appl
12	1485	79.2	478	2	US-09-383-916-8 Sequence 8, Appl
13	1486.5	79.2	453	2	US-09-301-593-18 Sequence 18, Appl
14	1485	79.2	462	2	US-09-627-896B-24 Sequence 24, Appl
15	1485	79.2	478	2	US-08-487-550-8 Sequence 8, Appl
16	1485	79.2	478	2	US-09-526-098-8 Sequence 8, Appl
17	1485	79.2	478	2	US-09-383-916-8 Sequence 8, Appl
18	1485	79.2	478	2	US-09-758-173-8 Sequence 8, Appl
19	1485	79.2	478	2	US-09-576-424-8 Sequence 8, Appl
20	1481.5	79.0	452	2	US-09-027-449-71 Sequence 71, Appl
21	1481.5	79.0	452	2	US-09-026-985-71 Sequence 71, Appl
22	1481.5	79.0	452	2	US-09-121-952A-71 Sequence 71, Appl
23	1481.5	79.0	452	2	US-09-234-340A-71 Sequence 71, Appl
24	1481.5	79.0	452	2	US-09-355-014-71 Sequence 71, Appl
25	1480.5	78.9	454	1	US-07-934-373C-22 Sequence 22, Appl
26	1480.5	78.9	454	2	US-08-437-642B-22 Sequence 22, Appl
27	1480.5	78.9	454	2	US-08-146-206C-22 Sequence 22, Appl

28	1480.5	78.9	454	2	US-09-705-686-22	Sequence 22, Appl
29	1480.5	78.9	454	2	US-09-705-392A-22	Sequence 22, Appl
30	1480.5	78.9	454	2	US-09-705-398-22	Sequence 22, Appl
31	1480.5	78.9	454	4	PCT-US93-07832-22	Sequence 22, Appl
32	1462	77.9	451	2	US-09-247-352-3	Sequence 3, Appl
33	1462	77.9	451	2	US-09-466-635-3	Sequence 3, Appl
34	1459.5	77.8	467	2	US-08-030-175-41	Sequence 41, Appl
35	1455.5	77.6	467	2	US-08-030-175-42	Sequence 42, Appl
36	1444	77.0	470	2	US-09-859-053-28	Sequence 28, Appl
37	1440.5	76.8	449	2	US-09-679-397-2	Sequence 2, Appl
38	1440.5	76.8	449	2	US-09-680-148-2	Sequence 2, Appl
39	1440.5	76.8	449	2	US-09-304-455A-2	Sequence 2, Appl
40	1440.5	76.8	449	2	US-10-356-974-2	Sequence 2, Appl
41	1436.5	76.3	467	1	US-07-916-098A-45	Sequence 45, Appl
42	1431.5	76.3	475	2	US-09-740-002-25	Sequence 25, Appl
43	1430	76.0	474	2	US-09-848-832-3	Sequence 3, Appl
44	1425.5	76.0	475	2	US-09-740-002-27	Sequence 27, Appl
45	1419	75.6	470	2	US-10-104-047-3730	Sequence 3730, Ap

ALIGNMENTS

RESULT 1  
US-09-238-741-4  
; Sequence 4, Application US/09238741  
; Patent No. 6897044  
; GENERAL INFORMATION:  
; APPLICANT: BRASLAWSKY, GARY R.  
; APPLICANT: HANNA, NABIL  
; APPLICANT: HARIHARAN, KANDASAMY  
; APPLICANT: LABARRE, MICHAEL J.  
; APPLICANT: HUYNH, TRI B.  
; TITLE OF INVENTION: PRODUCTION OF TETRAVALENT ANTIBODIES  
; FILE REFERENCE: 23522.0584  
; CURRENT APPLICATION NUMBER: US/09/238,741  
; CURRENT FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 470  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: "Dimeric" Anti-CD20 Heavy Chain (Version 1)  
US-09-238-741-4

Query Match		86.0%	Score 1613;	DB 2;	Length 470;
Best Local Similarity		67.7%;	Pred. No. 1.3e-115;		
Matches 318;		Conservative 13;	Mismatches 23;	Indels 116; Gaps 2;	
QY	1	MGWSLFLVAVATRVLSQVOLVSGAEVVGASVKISCKASGYTFTDTHATHWKONP	60		
DB	1	MGWSLFLVAVATRVLSQVOLVSGAEVVGASVKISCKASGYTFTSYNNHWKQTP	60		
QY	61	GORLEWIGYFSGNDDFKYNERFKGKATLTADTASTAYVELSSLRSEDTAVYFCTRSLN	120		
DB	61	GRGLEWIGAIYFGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYCARSTY	120		
QY	121	MA-----YWGQGLTVTVSSASTKGFSPFLAPSSKSTSGGTAAALGCLVKDYPPPTVVS	174		
DB	121	YGGDWYFNWVGAGTTVTVSAASTKGFSPFLAPSSKSTSGGTAAALGCLVKDYPPPTVVS	180		
QY	175	WNSGALTSGVHTFPVAVLOSGLYSLSVVTVVSSLSGTQTYICNVNHNKPSNTKVDKKVEP	234		
DB	181	WNSGALTSGVHTFPVAVLOSGLYSLSVVTVVSSLSGTQTYICNVNHNKPSNTKVDKKVEP	240		
QY	235	KSCDKTHTCPPCP-----	247		
DB	241	KSCDKTHTCPPCPAPELGGPSVFLPPKPKDTLMISRTPEVTVVVDVSHEDPEVKPNW	300		
QY	248	-----	247		

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Db 301 YDGVVEVNAKTPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
Qy 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 304
Db 361 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
Qy 305 LDSGSEFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 354
Db 421 LDSGSEFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470

RESULT 2
US-09-698-705-11
; Sequence 11, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koepfen, H.
; APPLICANT: Lasky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; FILE REFERENCE: P177R1
; CURRENT APPLICATION NUMBER: US/09/698,705
; PRIORITY FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 11
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is chimeric mouse/human
US-09-698-705-11

Query Match 83.1%; Score 1559; DB 2; Length 466;
Best Local Similarity 65.5%; Pred. No. 1.8e-111;
Matches 305; Conservative 21; Mismatches 28; Indels 112; Gaps 2;

Qy 1 MGSWLLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHHVKQNP 60
Db 1 MGSWLLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHHVKQNP 60
Qy 61 GORLEWIGYFSPGNDDFKYNRERFKGKATLTADTSASTAYVELSSLSRSEDYAVYFC-- 118
Db 61 GRGLEWIGRIDPSDSEIHYDQKDKATLTVDKSSSTAYIQLSSLTSEDSAVYCALTGI 120
Qy 119 LNAVYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSG 178
Db 121 YAMAYWGQGSTVTVSSAKTGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSG 180
Qy 179 ALTSGVHTFPVQLQSSGLYSLSVTVPSSSLGTQYICNVNHPKSNKTKVDKVPKSCD 238
Db 181 ALTSGVHTFPVQLQSSGLYSLSVTVPSSSLGTQYICNVNHPKSNKTKVDKVPKSCD 240
Qy 239 KHTHCPCPCP----- 247
Db 241 KHTHCPCPCPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVG 300
Qy 248 -----G 248
Db 301 VEVHNAKTPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAG 360
Qy 249 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD 308
Db 361 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD 420
Qy 309 GSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 354
Db 421 GSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 466
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RESULT 3
US-09-301-593-43
; Sequence 43, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John B.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 43
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-43

Query Match 82.6%; Score 1549; DB 2; Length 472;
Best Local Similarity 65.3%; Pred. No. 1e-110;
Matches 309; Conservative 15; Mismatches 29; Indels 120; Gaps 3;

Qy 1 MGSWLLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHHVKQNP 60
Db 1 MDWTWRVFCLLAVAPGAHSQVQLVQSGAEVVKPGASVKISCKTSRYTFTYTIHWVQAP 60
Qy 61 GORLEWIGYFSPGNDDFKYNRERFKGKATLTADTSASTAYVELSSLSRSEDYAVYFC-- 117
Db 61 GORLEWIGIGINPNNGIPNYNOKFKGRALITVVKSASTAYMELSSLSRSEDYAVYCARRI 120
Qy 118 -----SLNMAWGGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPV 171
Db 121 AVGYDEGHAMDYWGQGLTVTVSS--STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPV 179
Qy 172 TVSWNSGALTSGVHTFPVQLQSSGLYSLSVTVPSSSLGTQYICNVNHPKSNKTKVDK 231
Db 180 TVSWNSGALTSGVHTFPVQLQSSGLYSLSVTVPSSSLGTQYICNVNHPKSNKTKVDK 239
Qy 232 VEPKSCDKTHTCPPCP----- 247
Db 240 VEPKSCDKTHTCPPCPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 299
Qy 248 ----- 247
Db 300 FNNYVDGVEVHNAKTPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 359
Qy 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 301
Db 360 TTSKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 419
Qy 302 RPVLDSGSEFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 354
Db 420 RPVLDSGSEFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 472

RESULT 4
US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
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;; TITLE OF INVENTION: Humanized Antibodies Reactive with  
;; TITLE OF INVENTION: GPIIB/IIIA  
;; NUMBER OF SEQUENCES: 23  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: William M. Smith  
;; STREET: One Market Plaza, Steuart Tower, Suite 2000  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94105  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/458,516  
;; FILING DATE:  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/059,159  
;; FILING DATE: 03-MAY-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Smith, William M.  
;; REGISTRATION NUMBER: 30,223  
;; REFERENCE/DOCKET NUMBER: 11823-37-3  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-326-2400  
;; TELEFAX: 415-326-2422  
;; INFORMATION FOR SEQ ID NO: 13:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 449 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-458-516-13

Query Match 82.1%; Score 1541; DB 1; Length 449;  
Best Local Similarity 67.5%; Pred. No. 4e-110;  
Matches 303; Conservative 10; Mismatches 22; Indels 114; Gaps 2;  
QY 20 QVQLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNPQGLRWIGYFSGNDDFKY 79  
DB 1 QVQLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNPQGLRWIGYFSGNDDFKY 60  
QY 80 NERFKGKATLTADTSASTAYVELSLRSEDATVYFCTRSIN----MAYVQGGTLVTVSSA 135  
DB 61 NEKFKGRVLTVDENSTNTAYMELSLRSEDATVYFCARRDGNVGFAYWGQGGTLVTVSSA 120  
QY 136 STKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLQSSG 195  
DB 121 STKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLQSSG 180  
QY 196 LYSLSVSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCP----- 247  
DB 181 LYSLSVSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 240  
QY 248 ----- 247  
DB 241 SVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNPNVVDGVEVHNAKTKPREEQYNS 300  
QY 248 -----GQPREPQVYTLPPSRDEL 265  
DB 301 TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360  
QY 266 TRNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPPVLDSGSPFLYSKLTVDKSRWQ 325  
DB 361 TRNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPPVLDSGSPFLYSKLTVDKSRWQ 420  
QY 326 QGNVFSCSVHNEALHNHYTQKSLSLSPGK 354  
DB 421 QGNVFSCSVHNEALHNHYTQKSLSLSPGK 449

## RESULT 5

US-09-301-593-30  
; Sequence 30, Application US/09301593A  
; Patent No. 6455677  
; GENERAL INFORMATION:  
; APPLICANT: Park, John E.  
; APPLICANT: Garin-Chesa, Pilar  
; APPLICANT: Bamberger, Uwe  
; APPLICANT: Leger, Olivier  
; APPLICANT: Saldanha, Jose W.  
; APPLICANT: Rettig, Wolfgang J.  
; TITLE OF INVENTION: FAP-specific Antibody with Improved Productibility  
; FILE REFERENCE: 0652.1890001  
; CURRENT APPLICATION NUMBER: US/09/301,593A  
; CURRENT FILING DATE: 1999-04-29  
; EARLIER APPLICATION NUMBER: EP 98107925.4  
; EARLIER FILING DATE: 1998-04-30  
; EARLIER APPLICATION NUMBER: US 60/086,049  
; EARLIER FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 472  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-301-593-30

Query Match 81.2%; Score 1524; DB 2; Length 472;  
Best Local Similarity 63.8%; Pred. No. 8.5e-109;  
Matches 302; Conservative 20; Mismatches 31; Indels 120; Gaps 3;  
QY 1 MGMSLLFLVAVATRVLSQVLQVSGAEVVKPGASVKISKASGYTFDTHAIHWKQNP 60  
DB 1 MGMSVFLFLLSGTACGLSEVLQVSGAEVVKPGASVKISKASGYTFDTHAIHWKQNP 60  
QY 61 GORLEWIGYFSGNDDFKYNRPFKATLTADTSASTAYVELSLRSEDATVYFCTR--- 117  
DB 61 GKSLEWIGGINPNNGIPNYPNQFKGRATLTVGKSSSTAYMELSLRSEDATVYFCARRRI 120  
QY 118 -----SLNMAVWGQGLTVTVSSASTKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPV 171  
DB 121 AVYDEGHAMDYWGQGTSTVTVSS-STKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPV 179  
QY 172 TVSWNSGALTSGVHTTFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKK 231  
DB 180 TVSWNSGALTSGVHTTFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKK 239  
QY 232 VEPKSCDKTHTCPPCP----- 247  
DB 240 VEPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 299  
QY 248 ----- 247  
DB 300 FNNYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 359  
QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 301  
DB 360 TTSKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 419  
QY 302 PPLVDSGSPFLYSKLTVDKSRWQGNVFPSCSVHNEALHNHYTQKSLSLSPGK 354  
DB 420 PPLVDSGSPFLYSKLTVDKSRWQGNVFPSCSVHNEALHNHYTQKSLSLSPGK 472

## RESULT 6

US-10-104-047-3329  
; Sequence 3329, Application US/10104047  
; Patent No. 6943241  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. 6943241el full length cdna

```
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3329
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3329

Query Match      80.5%; Score 1509.5; DB 2; Length 489;
Best Local Similarity 60.9%; Pred. No. 1.1e-107;
Matches 298; Conservative 21; Mismatches 35; Indels 135; Gaps 2;

QY 1 MGSLLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNP 60
DB 1 MDWTRVFCLLAVAGAHSQVQLVQSGAEVVKPGASVRVSCAFGFTFTYQIHWVRQAP 60
QY 61 GQRLEWIGYFSPGNDDFKYNRPFGKATLTADTSASTAYVELSSLRASEDTAVYFCTR--- 117
DB 61 GQGLEWVGVSFPGGSATYAQRFGQRTVITRDTSTSTVTMDLDSLRSDDSAVYICARVVS 120
QY 118 -----SLNWAYWGQGLTLTVSSASTKGPSVFPFLAPSSKSTSGG 155
DB 121 ELFSFGGGTLTLDRIKVPNNHYSYGMVWGQGLTVTVSSASTKGPSVFPFLAPSSKSTSGG 180
QY 156 TAAAGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTPVPSLSLTQTY 215
DB 181 TAAAGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTPVPSLSLTQTY 240
QY 216 ICNVNHPKNTKVDKVEPKSCDKHTCTCPCP----- 247
DB 241 ICNVNHPKNTKVDKVEPKSCDKHTCTCPCPAPPELLGGPSVFLPFPKPKDTLMISRTPE 300
QY 248 ----- 247
DB 301 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE 360
QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 285
DB 361 YKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIA 420
QY 286 VEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQ 345
DB 421 VEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQ 480
QY 346 KSLSLSPGK 354
DB 481 KSLSLSPGK 489

RESULT 7
US-08-378-939-10
; Sequence 10, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-939-10

Query Match      80.3%; Score 1506; DB 1; Length 476;
Best Local Similarity 63.4%; Pred. No. 2.1e-107;
Matches 302; Conservative 20; Mismatches 32; Indels 122; Gaps 3;

QY 1 MGSLLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNP 60
DB 1 MDWTRFLFVVAATGVQSQMVQSGAEVVKPGSVTVSCASGSGTFSYAISWVRQAP 60
QY 61 GQRLEWIGYFSPGNDDFKYNRPFGKATLTADTSASTAYVELSSLRASEDTAVYFCT--- 116
DB 61 GQGLEWVGIIPLFGTPTYSQNFQGRVTITADKSTSTAHMELTSURSEDVAVYCATDRY 120
QY 117 RSLNWAY-----WGQGLTVTVSSASTKGPSVFPFLAPSSKSTSGTAAAGCLVKDYFP 168
DB 121 ROANFDRARVGVDFWPGQGLTVTVSSASTKGPSVFPFLAPSSKSTSGTAAAGCLVKDYFP 180
QY 169 EPTVTSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTPVPSLSLTQTYICNVNHPKNTKV 228
DB 181 EPTVTSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTPVPSLSLTQTYICNVNHPKNTKV 240
QY 229 DKKVEPKSCDKHTCTCPCP----- 247
DB 241 DKKVEPKSCDKHTCTCPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDP 300
QY 248 ----- 247
DB 301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 298
DB 361 IEKTIISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 420
QY 299 KTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKLSLSLSPGK 354
DB 421 KTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKLSLSLSPGK 476

RESULT 8
US-09-485-737B-67
; Sequence 67, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
```

;  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC  
US-09-485-7378-67

QY 314 YSKLTVDKSRWQGNVFSCSVMEALHNHYTKQSLSLSPGK 354  
|||  
Db 427 YSKLTVDKSRWQGNVFSCSVMEALHNHYTKQSLSLSPGK 467

RESULT 10  
 US-09-485-737B-90  
 ; Sequence 90, Application US/09485737B  
 ; Patent No. 6350860  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Buysee, Marie-Ange  
 ; APPLICANT: Sablon, Erwin  
 ; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,  
 ; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS  
 ; FILE REFERENCE: INNS:015  
 ; CURRENT APPLICATION NUMBER: US/09/485,737B  
 ; CURRENT FILING DATE: 2000-02-14  
 ; PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
 ; PRIOR FILING DATE: 1998-08-14  
 ; PRIOR APPLICATION NUMBER: EPO 98870139.7  
 ; PRIOR FILING DATE: 1998-06-18  
 ; PRIOR APPLICATION NUMBER: EPO 97870122.5  
 ; PRIOR FILING DATE: 1997-08-18  
 ; NUMBER OF SEQ ID NOS: 104  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 90  
 ; LENGTH: 711  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:

```

; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90

Query Match      80.0%; Score 1501; DB 2; Length 711;
Best Local Similarity 63.8%; Pred. No. 8.2e-107;
Matches 294; Conservative 24; Mismatches 31; Indels 112; Gaps 2

Qy 6 ILLPLVAVATRVLSQVLVQSGAEVVKPGASVKISKASGYTFTHAIHWKQNGORLE 65
Db 7 IFSLLISASVLSQVLVQSGSELKKPGASVKISKASGYTFTHDGMNWKQAFQOGLK 66
Qy 66 WIGVFSPCNDDFKNERFKGKATLTADTASATYVELSLRSEDYAVFPCTRS--LNMA 123
Db 67 WMGHWNTYTGSTVVDDEFKGRFVSLDTISVSNAYLIQISLKAEDTATYFCARRGFVMDY 126
Qy 124 WQQTLLVTVSSASTKGPSVFFPLAPLSKSTSGTGAALGCLVLDYFPPEPTVTVSNNGALTS 183
Db 127 WQQTLLVTVSSASTKGPSVFFPLAPLSKSTSGTGAALGCLVLDYFPPEPTVTVSNNGALTS 186
Qy 184 VHTPEAVLQSSGLYSLSSVTVTPSSSLGTQTVICNVNHPKSNTKVDKVKPEKSCDKTHTC 243
Db 187 VHTPEAVLQSSGLYSLSSVTVTPSSSLGTQTVICNVNHPKSNTKVDKVKPEKSCDKTHTC 246
Qy 244 PPCP----- 247
Db 247 PPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHN 306
Qy 248 ----- 309
Db 307 AKTKPRBEQYNSTYRVWVSLTVLHODWLNGKEYCKVSNKALPAPISEKTIISKAGQPRE 366
Qy 254 QVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPL 313
Db 367 QVYTLPPSRDEMTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPL 426
Qy 314 YSKLTVDKSRWQOQGVNFSCSVNHEALHNHYTQKSLSLSPGK 354
Db 427 YSKLTVDKSRWQOQGVNFSCSVNHEALHNHYTQKSLSLSPGK 467

RESULT 11
US-10-071-485-90
; Sequence 90, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buysse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERPERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SEQ ID NO 90
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-90

Query Match      80.0%; Score 1501; DB 2; Length 711;
Best Local Similarity 63.8%; Pred. No. 8.2e-107;

```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGTUT11
; CLONE: 2747531
; US-09-049-672A-8

Query Match          79.7%; Score 1495.5; DB 2; Length 467;
Best Local Similarity 63.3%; Pred. No. 1.3e-106;
Matches 292; Conservative 26; Mismatches 30; Indels 113; Gaps 2;

QY 7 LFLVAVATVLSQVQLVQSGAEVVRPGASVKISKASGYTFDTHAIHWKQNPQGORLEW 66
Db 7 ILFLVAAATCTHAQVQLVQSGAEVVRPGASVKISKASGYTFDTHAIHWKQNPQGORLEW 66
QY 67 IGVFSGNDGPKNERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTR---SLNWAY 123
Db 67 MGLAPENGAEVYAKFLGRLTLSEDTADTAYMFLNLLGSEDSAIYICARQHYDFFDF 126
QY 124 WGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 183
Db 127 WGGTMTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 186
QY 184 VHTFPAVLOSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVPEKSCDKHTHC 243
Db 187 VHTFPAVLOSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVPEKSCDKHTHC 246
QY 244 PCPP----- 247
Db 247 PPCPAPELGGPSVFILPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 306
QY 248 -----GQPREP 253
Db 307 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREP 366
QY 254 QVYTLPPSDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 313
Db 367 QVYTLPPSDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 426
QY 314 YSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSPGK 354
Db 427 YSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSPGK 467

RESULT 13
US-09-301-593-18
; Sequence 18, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652,1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent In Ver. 2.0

Query Match          79.2%; Score 1486.5; DB 2; Length 453;
Best Local Similarity 64.7%; Pred. No. 6.1e-106;
Matches 293; Conservative 16; Mismatches 25; Indels 119; Gaps 2;

QY 21 VOLVSGAEVVRPGASVKISKASGYTFDTHAIHWKQNPQGORLEWIGYFSPGNDGPKYN 80
Db 1 VOLQSGPELVKPGASVKMSCKTSRYTFTEYTIHWVRQSHGKSLWIGGINPNNGLPNYN 60
QY 81 ERFKGAATLTADTSASTAYVELSLRSEDYAVYFCTR-----SLNWAYGQGTTLVT 131
Db 61 QKFKGRATLTGKSSSTAYMELSLTSEDSAVVFCARRRIAYGYDEGHAMDYWGQTSVT 120
QY 132 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVL 191
Db 121 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVL 180
QY 192 QSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVPEKSCDKHTHTCPPCP--- 247
Db 181 QSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVPEKSCDKHTHTCPPCPAPEL 240
QY 248 ----- 247
Db 241 LGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTPREE 300
QY 248 -----GQPREPQVYTLPPS 261
Db 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPS 360
QY 262 RDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 321
Db 361 REEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
QY 322 SRWQQGNVFCSCVMHEALHNYHTQKSLSPGK 354
Db 421 SRWQQGNVFCSCVMHEALHNYHTQKSLSPGK 453

RESULT 14
US-09-627-896B-24
; Sequence 24, Application US/09627896B
; Patent No. 6827934
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702.0081-01000
; CURRENT APPLICATION NUMBER: US/09/627,896B
; CURRENT FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 24
; LENGTH: 462
; TYPE: PRT
; ORGANISM: 3D1 heavy chain
; US-09-627-896B-24

Query Match          79.2%; Score 1485; DB 2; Length 462;
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```
Best Local Similarity 63.9%; Pred. No. 8.1e-106;
Matches 297; Conservative 21; Mismatches 33; Indels 114; Gaps 4;

QY 1 MGSLLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHIVWKQP 60
Db 1 MGSLLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHIVWKQP 60
QY 61 GQRLHWIGVFGNDGFKNERFKGKATLTADTSASTAYVEISLSLASEDTAVYFCTRS- 119
Db 61 GQRLHWIGVFGNDGFKNERFKGKATLTADTSASTAYVEISLSLASEDTAVYFCTRS- 119
QY 120 NNAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGA 179
Db 120 NNAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGA 179
QY 121 YMDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGA 180
Db 121 YMDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGA 180
QY 180 LFGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNNVHKPSNT-KVDKKEPKSCD 238
Db 180 LFGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNNVHKPSNT-KVDKKEPKSCD 238
QY 181 LFGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNNVHKPSNT-KVDKKEPKSCD 240
Db 181 LFGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNNVHKPSNT-KVDKKEPKSCD 240
QY 239 KTHTCPPCP----- 247
Db 239 KTHTCPPCP----- 247
QY 241 E---CPPCPAPPAAAPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDG 297
Db 241 E---CPPCPAPPAAAPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDG 297
QY 248 -----GQ 249
Db 248 -----GQ 249
QY 298 EVHNAKTKPREQFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPAPIEKTISKTKGQ 357
Db 298 EVHNAKTKPREQFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPAPIEKTISKTKGQ 357
QY 250 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 309
Db 250 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 309
QY 358 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 417
Db 358 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 417
QY 310 SPFLYSKLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 354
Db 310 SPFLYSKLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 354
QY 418 SPFLYSKLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 462
Db 418 SPFLYSKLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 462

RESULT 15
US-08-487-550-8
; Sequence 8, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLSCULE TYPE: protein
US-08-487-550-8

Query Match 79.2%; Score 1485; DB 2; Length 478;
Best Local Similarity 61.1%; Pred. No. 8.4e-106;
Matches 292; Conservative 25; Mismatches 37; Indels 124; Gaps 3;

QY 1 MGSLLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHIVWKQP 60
Db 1 MGSLLILFLVAVATRVQCEVLVESGGGLVQPGSLRVSCAVSGFTTSDHYMYFRQAP 60
QY 61 GQRLHWIGVFGNDGFKNERFKGKATLTADTSASTAYVEISLSLASEDTAVYFCTRS 118
Db 61 GQRLHWIGVFGNDGFKNERFKGKATLTADTSASTAYVEISLSLASEDTAVYFCTRS 118
QY 61 GQRLHWIGVFGNDGFKNERFKGKATLTADTSASTAYVEISLSLASEDTAVYFCTRS 120
Db 61 GQRLHWIGVFGNDGFKNERFKGKATLTADTSASTAYVEISLSLASEDTAVYFCTRS 120
QY 119 L-----NNAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 166
Db 119 L-----NNAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 166
QY 121 YISHCRGGVYGGYFEPFPGQALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
Db 121 YISHCRGGVYGGYFEPFPGQALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
QY 167 FPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNNVHKPSNT 226
Db 167 FPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNNVHKPSNT 226
QY 181 FPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNNVHKPSNT 240
Db 181 FPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNNVHKPSNT 240
QY 227 KYDKKVEPKSCDKTHCTCPCP----- 247
Db 227 KYDKKVEPKSCDKTHCTCPCP----- 247
QY 241 KVDKKAEPKSCDKTHCTCPCPAPPELLGPGSVFLPPPKDPTLMISRTPEVTCVVVDVSH 300
Db 241 KVDKKAEPKSCDKTHCTCPCPAPPELLGPGSVFLPPPKDPTLMISRTPEVTCVVVDVSH 300
QY 248 ----- 247
Db 248 ----- 247
QY 301 DPEVKFNWYVDGVEVHNAKTKPREEQFNSTFRVSVLTVVHODWLNKGEYKCKVSNKALP 360
Db 301 DPEVKFNWYVDGVEVHNAKTKPREEQFNSTFRVSVLTVVHODWLNKGEYKCKVSNKALP 360
QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 296
Db 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 296
QY 361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
Db 361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
QY 297 NYKTTTPVLDSDGSPFLYSKLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 354
Db 297 NYKTTTPVLDSDGSPFLYSKLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 354
QY 421 NYKTTTPVLDSDGSPFLYSKLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 478
Db 421 NYKTTTPVLDSDGSPFLYSKLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 478

Search completed: February 16, 2006, 10:25:01
Job time : 42.3333 secs
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GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.  
 OM protein - protein search, using sw model  
 Run on: February 16, 2006, 10:12:11 ; Search time 182.96 Seconds  
 (without alignments)  
 1365.094 Million cell updates/sec  
 Title: US-10-058-069-7  
 Perfect score: 1876  
 Sequence: 1 MGWSLILFLNAVATRVLSQ.....MHEALNHVTKSLSLSPGK 354

Scoring table: BLOSUM62.  
 Gapop 10.0 , Gapext 0.5  
 Searched: 2166443 seqs, 705528306 residues  
 Total number of hits satisfying chosen parameters: 2166443  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries  
 Database : Uniprot\_05.80.\*  
 1: uniprot\_sprot.\*  
 2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Query		Match		Length		DB		ID		Description	
Result No.	Score	Match	%	Length	DB	ID	Score	Match	%	Length	DB	ID	Score	Match	%
1	1521.5	81.1	469	2	Q7Z7P5	HUMAN	Q7Z7P5	homo sapien	Q6mz7	homo sapien	Q6mz7	homo sapien	Q6mz7	homo sapien	Q6mz7
2	1500.5	80.0	475	2	Q6N095	HUMAN	Q6N095	homo sapien	Q6mz6	homo sapien	Q6mz6	homo sapien	Q6mz6	homo sapien	Q6mz6
3	1479	78.8	480	2	Q6P1F1	HUMAN	Q6P1F1	homo sapien	Q6p1f1	homo sapien	Q6p1f1	homo sapien	Q6p1f1	homo sapien	Q6p1f1
4	1457.5	77.7	469	2	Q569F4	HUMAN	Q569F4	homo sapien	Q569f4	homo sapien	Q569f4	homo sapien	Q569f4	homo sapien	Q569f4
5	1452.5	77.4	475	2	Q5E8E5	HUMAN	Q5E8E5	homo sapien	Q5e8e5	homo sapien	Q5e8e5	homo sapien	Q5e8e5	homo sapien	Q5e8e5
6	1440	76.8	472	2	Q6N089	HUMAN	Q6N089	homo sapien	Q6n089	homo sapien	Q6n089	homo sapien	Q6n089	homo sapien	Q6n089
7	1439	76.7	518	2	Q6N030	HUMAN	Q6N030	homo sapien	Q6n030	homo sapien	Q6n030	homo sapien	Q6n030	homo sapien	Q6n030
8	1430.5	76.3	475	2	Q6M2Q6	HUMAN	Q6M2Q6	homo sapien	Q6m2q6	homo sapien	Q6m2q6	homo sapien	Q6m2q6	homo sapien	Q6m2q6
9	1427.5	76.1	544	2	Q6P195	HUMAN	Q6P195	homo sapien	Q6p195	homo sapien	Q6p195	homo sapien	Q6p195	homo sapien	Q6p195
10	1426	76.0	466	2	Q6IN78	HUMAN	Q6IN78	homo sapien	Q6in78	homo sapien	Q6in78	homo sapien	Q6in78	homo sapien	Q6in78
11	1425	76.0	470	2	Q6P1A4	HUMAN	Q6P1A4	homo sapien	Q6p1a4	homo sapien	Q6p1a4	homo sapien	Q6p1a4	homo sapien	Q6p1a4
12	1422.5	75.8	475	2	Q6GNW7	HUMAN	Q6GNW7	homo sapien	Q6gnw7	homo sapien	Q6gnw7	homo sapien	Q6gnw7	homo sapien	Q6gnw7
13	1417	75.5	466	2	Q6N096	HUMAN	Q6N096	homo sapien	Q6n096	homo sapien	Q6n096	homo sapien	Q6n096	homo sapien	Q6n096
14	1411.5	75.2	475	2	Q5RE17	PONPY	Q5RE17	pongo pygma	Q5re17	pongo pygma	Q5re17	pongo pygma	Q5re17	pongo pygma	Q5re17
15	1410	75.2	478	2	Q6P181	HUMAN	Q6P181	homo sapien	Q6p181	homo sapien	Q6p181	homo sapien	Q6p181	homo sapien	Q6p181
16	1407.5	75.0	473	2	Q6M2V7	HUMAN	Q6M2V7	homo sapien	Q6m2v7	homo sapien	Q6m2v7	homo sapien	Q6m2v7	homo sapien	Q6m2v7
17	1402	74.7	480	2	Q6N094	HUMAN	Q6N094	homo sapien	Q6n094	homo sapien	Q6n094	homo sapien	Q6n094	homo sapien	Q6n094
18	1400	74.6	482	2	Q7Z351	HUMAN	Q7Z351	homo sapien	Q7z351	homo sapien	Q7z351	homo sapien	Q7z351	homo sapien	Q7z351
19	1398.5	74.5	473	2	Q6P055	HUMAN	Q6P055	homo sapien	Q6p055	homo sapien	Q6p055	homo sapien	Q6p055	homo sapien	Q6p055
20	1392	74.2	470	2	Q7Z5W1	HUMAN	Q7Z5W1	homo sapien	Q7z5w1	homo sapien	Q7z5w1	homo sapien	Q7z5w1	homo sapien	Q7z5w1
21	1388.5	74.0	519	2	Q5E8M2	HUMAN	Q5E8M2	homo sapien	Q5e8m2	homo sapien	Q5e8m2	homo sapien	Q5e8m2	homo sapien	Q5e8m2
22	1379.5	73.5	465	2	Q6GNX6	HUMAN	Q6GNX6	homo sapien	Q6gnx6	homo sapien	Q6gnx6	homo sapien	Q6gnx6	homo sapien	Q6gnx6
23	1377.5	73.4	481	2	Q6N097	HUMAN	Q6N097	homo sapien	Q6n097	homo sapien	Q6n097	homo sapien	Q6n097	homo sapien	Q6n097
24	1374	73.2	476	2	Q6GNK1	HUMAN	Q6GNK1	homo sapien	Q6gnk1	homo sapien	Q6gnk1	homo sapien	Q6gnk1	homo sapien	Q6gnk1
25	1330	70.9	464	2	Q6MZU6	HUMAN	Q6MZU6	homo sapien	Q6mzu6	homo sapien	Q6mzu6	homo sapien	Q6mzu6	homo sapien	Q6mzu6
26	1332	70.5	470	2	Q68CN4	HUMAN	Q68CN4	homo sapien	Q68cn4	homo sapien	Q68cn4	homo sapien	Q68cn4	homo sapien	Q68cn4
27	1285.5	68.5	465	2	Q6P6C4	HUMAN	Q6P6C4	homo sapien	Q6p6c4	homo sapien	Q6p6c4	homo sapien	Q6p6c4	homo sapien	Q6p6c4
28	1284.5	68.5	521	2	Q8N4Y9	HUMAN	Q8N4Y9	homo sapien	Q8n4y9	homo sapien	Q8n4y9	homo sapien	Q8n4y9	homo sapien	Q8n4y9
29	1219	65.0	458	2	Q5BJZ2	RAT	Q5BJZ2	rattus norv	Q5bjz2	rattus norv	Q5bjz2	rattus norv	Q5bjz2	rattus norv	Q5bjz2
30	1218	64.9	417	2	Q6N093	HUMAN	Q6N093	homo sapien	Q6n093	homo sapien	Q6n093	homo sapien	Q6n093	homo sapien	Q6n093
31	1205	64.2	473	2	Q8TC63	HUMAN	Q8TC63	homo sapien	Q8tc63	homo sapien	Q8tc63	homo sapien	Q8tc63	homo sapien	Q8tc63

32	1195.5	63.7	476	2	Q6MXZ7	HUMAN	Q6mxz7	homo sapien	Q6mxz7	homo sapien	Q6mxz7	homo sapien	Q6mxz7	homo sapien	Q6mxz7
33	1162	61.9	348	2	Q6PYX1	HUMAN	Q6pyx1	homo sapien	Q6pyx1	homo sapien	Q6pyx1	homo sapien	Q6pyx1	homo sapien	Q6pyx1
34	1148.5	61.2	465	2	Q6FJB2	MOUSE	Q6fjb2	mus musculus	Q6fjb2	mus musculus	Q6fjb2	mus musculus	Q6fjb2	mus musculus	Q6fjb2
35	1148	61.2	458	2	Q5BK05	RAT	Q5bk05	rattus norv	Q5bk05	rattus norv	Q5bk05	rattus norv	Q5bk05	rattus norv	Q5bk05
36	1138.5	60.7	473	2	Q9DBL4	MOUSE	Q9dbl4	mus musculus	Q9dbl4	mus musculus	Q9dbl4	mus musculus	Q9dbl4	mus musculus	Q9dbl4
37	1121.5	59.8	463	2	Q99LC4	MOUSE	Q99lc4	mus musculus	Q99lc4	mus musculus	Q99lc4	mus musculus	Q99lc4	mus musculus	Q99lc4
38	1116	59.5	330	1	IGHG1	HUMAN	IGHG1	homo sapien	IGHG1	homo sapien	IGHG1	homo sapien	IGHG1	homo sapien	IGHG1
39	1107	59.0	468	2	Q569W9	MOUSE	Q569w9	mus musculus	Q569w9	mus musculus	Q569w9	mus musculus	Q569w9	mus musculus	Q569w9
40	1101	58.7	470	2	Q77MK1	MOUSE	Q77mk1	mus musculus	Q77mk1	mus musculus	Q77mk1	mus musculus	Q77mk1	mus musculus	Q77mk1
41	1100	58.6	464	2	Q6PF95	MOUSE	Q6pf95	mus musculus	Q6pf95	mus musculus	Q6pf95	mus musculus	Q6pf95	mus musculus	Q6pf95
42	1096	58.4	472	2	Q6PJA7	MOUSE	Q6pja7	mus musculus	Q6pja7	mus musculus	Q6pja7	mus musculus	Q6pja7	mus musculus	Q6pja7
43	1087.5	58.0	487	2	Q6SZL2	9MURI	Q6szl2	mus sp. fv/	Q6szl2	mus sp. fv/	Q6szl2	mus sp. fv/	Q6szl2	mus sp. fv/	Q6szl2
44	1083.5	57.8	477	2	Q58E56	MOUSE	Q58e56	mus musculus	Q58e56	mus musculus	Q58e56	mus musculus	Q58e56	mus musculus	Q58e56
45	1058	56.4	468	2	Q505N9	MOUSE	Q505n9	mus musculus	Q505n9	mus musculus	Q505n9	mus musculus	Q505n9	mus musculus	Q505n9

# ALIGNMENTS

RESULT 1  
 Q7Z7P5 HUMAN  
 ID Q7Z7P5 HUMAN PRELIMINARY; PRT; 469 AA.  
 AC Q7Z7P5;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE IGHG1 protein.  
 GN Name=IGHG1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzyzinski M.I., Skalka U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RG NIH MGC Project;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC051328; AAHS1328.1; -; mRNA.  
 DR HSSP; P01857; 1H2H.  
 DR SMR; Q7Z7P5; 20-469.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF07654; C1-set; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.



KW Immunoglobulin domain.  
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;  
Query Match 81.1%; Score 1521.5; DB 2; Length 469;  
Best Local Similarity 64.0%; Pred. No. 2.9e-101;  
Matches 300; Conservative 21; Mismatches 33; Indels 115; Gaps 3;  
QY 1 MWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60  
DB 1 MDWTSILFLVAATGARFQVHLVQSGAEVVKPGASVKLSCKTSGYNFSYDLIWRQAP 60  
QY 61 GORLEWIGVPSGNDDFKYNRFKPKATLTADTSASTAYVELSLRSEDATVFC-TRSL 119  
DB 61 GQGLEWGMWISAHNGDTKARKFQGRVTWTTDSATTSYWFPSRLSDDTALFYCATKSR 120  
QY 120 NMA----YNGQGTFLVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSW 175  
DB 121 GQVGDPSGQGTFLVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSW 180  
QY 176 NSGALTSGVHTPAPVQLQSSGLYSLSVWTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPK 235  
DB 181 NSGALTSGVHTPAPVQLQSSGLYSLSVWTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPK 240  
QY 236 SCDKTHTCPPCP----- 247  
DB 241 SCDKTHTCPPCPAPPELLGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWY 300  
QY 248 ----- 247  
DB 301 VDGVEVHNAKTPREBQYNSYTRVWSVLTVLHQLDNLNGKEYCKVSNKALPAPIETKISK 360  
QY 248 --GQPEPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVESNGQPENNYKTPPVVL 305  
DB 361 AKGQPEPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVESNGQPENNYKTPPVVL 420  
QY 306 DSDGSFLLSKLTVDSKRWQGNVFCVSMVHEALHNHYTKSLSPGK 354  
DB 421 DSDGSFLLSKLTVDSKRWQGNVFCVSMVHEALHNHYTKSLSPGK 469

RESULT 2  
Q6N095 HUMAN  
ID Q6N095\_HUMAN PRELIMINARY; PRT; 475 AA.  
AC Q6N095  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686K03196;  
GN Names=DKFZp686K03196;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Esophagus tumor;  
RG The German CDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640621; CAE45775.1; -, mRNA.  
DR HSSP; P01861; IADQ.  
DR SMR; Q6N095; 20-475.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 3.  
DR SMART; SM00406; IGv; 1.

DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 475 AA; 52360 MW; 7BA14104CD2DB8F0 CRC64;  
Query Match 80.0%; Score 1500.5; DB 2; Length 475;  
Best Local Similarity 62.3%; Pred. No. 9.7e-100;  
Matches 296; Conservative 24; Mismatches 34; Indels 121; Gaps 2;  
QY 1 MWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60  
DB 1 MDWTSILFLVAATGARFQVHLVQSGAEVVKPGASVKLSCKTSGYNFSYDLIWRQAP 60  
QY 61 GORLEWIGVPSGNDDFKYNRFKPKATLTADTSASTAYVELSLRSEDATVFC-TRSL 120  
DB 61 GORLEWGMWISAHNGDTKARKFQGRVTWTTDSATTSYWFPSRLSDDTALFYCATKSR 120  
QY 121 NMA----YNGQGTFLVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE 169  
DB 121 GRALWFGELDAFDINGQGTFLVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE 180  
QY 170 PVTVSNWNGALTSGVHTPAPVQLQSSGLYSLSVWTVPPSSSLGTQTYICNVNHKPSNTKVD 229  
DB 181 PVTVSNWNGALTSGVHTPAPVQLQSSGLYSLSVWTVPPSSSLGTQTYICNVNHKPSNTKVD 240  
QY 230 KKEVPEKCDKTHTCPPCP----- 247  
DB 241 KKEVPEKCDKTHTCPPCPAPPELLGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPE 300  
QY 248 ----- 247  
DB 301 VKFNWYVDGVEVHNAKTPREBQYNSYTRVWSVLTVLHQLDNLNGKEYCKVSNKALPAPI 360  
QY 248 --GQPEPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVESNGQPENNYK 299  
DB 361 EKTISKAKGQPEPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVESNGQPENNYK 420  
QY 300 TTPPVLDSDGSFLLSKLTVDSKRWQGNVFCVSMVHEALHNHYTKSLSPGK 354  
DB 421 TTPPVLDSDGSFLLSKLTVDSKRWQGNVFCVSMVHEALHNHYTKSLSPGK 475

RESULT 3  
Q6PJF1 HUMAN  
ID Q6PJF1\_HUMAN PRELIMINARY; PRT; 480 AA.  
AC Q6PJF1  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RG MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McQuellan J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,



Db 421 TTPPVLDSGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 475

```
RESULT 5
QSEFES HUMAN
ID QSEFES_HUMAN PRELIMINARY; PRT; 475 AA.
AC QSEFES;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Anti-RND monoclonal T125 gamma1 heavy chain precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaucher C., Klein P., Belliard R.;
RT "Sequence determination of the recombinant human anti-Rhd monoclonal
RT antibody T125."
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY894992; AAW82028.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS0290; IG_MHC; UNKNOWN_2.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
FT CHAIN.
SQ SEQUENCE 475 AA; 52362 MW; 1367D40DC7D2859 CRC64;

Query Match 77.4%; Score 1452.5; DB 2; Length 475;
Best Local Similarity 60.2%; Pred. No. 2.8e-96;
Matches 286; Conservative 27; Mismatches 41; Indels 121; Gaps 2;

QY 1 MGSLILLFLVAVATVLSQVLQVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60
DB 1 MEFGLSWFLVALLRGVQCVQLVESGGGVQGRSLRSLCTASGTFKYNIAHWVRQAP 60

QY 61 GORLEWIGYFSPGNDPFKYNERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRSLN 120
DB 61 AKGLEWVAISYDGRNIQYADSVKGRCTPSRDNSQDTLVLQNSLRPEDYAVYCARPVR 120

QY 121 MAY-----WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE 169
DB 121 SRWLQGLGDAFHNGOGTMTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE 180

QY 170 PVTVSNWNSGALTSVGHVTPFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVD 229
DB 181 PVTVSNWNSGALTSVGHVTPFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVD 240

QY 230 KKVEPKSCDKHTCTCPCP----- 247
DB 241 KKVEPKSCDKHTCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 300

QY 248 ----- 247
DB 301 VKFNWTVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPI 360

QY 248 -----GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEHESNGQPENNYK 299
DB 361 EKTISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEHESNGQPENNYK 420

QY 300 TTPPVLDSGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 354
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## RESULT 6

```
Q6N089 HUMAN
ID Q6N089_HUMAN PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAE45781.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS0290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D00046D279 CRC64;

Query Match 76.8%; Score 1440; DB 2; Length 472;
Best Local Similarity 59.3%; Pred. No. 2.2e-95;
Matches 280; Conservative 33; Mismatches 41; Indels 118; Gaps 2;

QY 1 MGSLILLFLVAVATVLSQVLQVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60
DB 1 MELGLTWIFLLAILKGVQCEVLVSGGGLVQVQGRSLRSLCAASGTFDDYIAHWVRQAP 60

QY 61 GORLEWIGYFSPGNDPFKYNERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRSL- 119
DB 61 GKGLEWVSGISWNSGSIAYADSVKGRFTISRDNKNSLVLQNSLRAEDTALYYCAKEIG 120

QY 120 -----NNAVYQGGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT 172
DB 121 AHNFYVYGVDMVQGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT 180

QY 173 VSNWNSGALTSVGHVTPFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKV 232
DB 181 VSNWNSGALTSVGHVTPFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKRV 240

QY 233 EPKSCDKHTCTCPCP----- 247
DB 241 EPKSCDKHTCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 300

QY 248 ----- 247
DB 301 NWVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIEKT 360

QY 248 -----GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEHESNGQPENNYK 302
DB 361 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEHESNGQPENNYK 420

QY 303 PVLDSGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 354
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QY 248 ----- 247
DB 301 VKFNHYVDGVEVHNAKTPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 360
QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYK 299
DB 361 EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYK 420
QY 300 TTPPVLDSDGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 354
DB 421 TTPPVLDSDGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 475

RESULT 9
Q6PJ95 HUMAN
ID Q6PJ95 HUMAN PRELIMINARY; PRT; 544 AA.
AC Q6PJ95
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshitaki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019046; AAH19046.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR SWR; Q6PJ95; 20-473.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig-v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 544 AA; 60102 MW; 18959814B2237C668 CRC64;

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Query Match 76.1%; Score 1427.5; DB 2; Length 544;

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Best Local Similarity 59.6%; Pred. No. 2.1e-94;
Matches 282; Conservative 28; Mismatches 42; Indels 121; Gaps 2;
QY 1 MGWSLILFLVAVATRVLSQVQLVOSGAEVVKPGASVKISKASGYTTDDTHAIHWKQNP 60
DB 1 MEFGLSVFLVALLRGVQCQALVSGGGVQVPGSSLRSLSCAASGRFNSYGMHWVRQAP 60
QY 61 GORLEWIGVFSQNDDFKYNRFKSKATLTADTSATAVVELSLRSSEDTAVVFCTRS-- 118
DB 61 KGLEWAVAFVSDESKYAAASVKGRFTISRNSKNVLSLQNSLRVEDTAVYICAKOOK 120
QY 119 -----LNMYMGQGLTVTVSSASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPE 169
DB 121 PHSNSWFLTFNDSWGRGTLTVSSASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPE 180
QY 170 PVTSMNSGALTSGVHTTTPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKNTKVD 229
DB 181 PVTSMNSGALTSGVHTTTPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKNTKVD 240
QY 230 KKEPKSCDKTHTCPCP----- 247
DB 241 KKEPKSCDKTHTCPCPAPELLGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPE 300
QY 248 ----- 247
DB 301 VKFNHYVDGVEVHNAKTPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 360
QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYK 299
DB 361 EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYK 420
QY 300 TTPPVLDSDGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSP 352
DB 421 TTPPVLDSDGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSP 473

RESULT 10
Q6IN78 HUMAN
ID Q6IN78 HUMAN PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshitaki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
TX TISSUE=Primary B-Cells;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.O., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR SMR; Q6FJA4; 20-470.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50854 MW; 53EB0BCEDE81076E CRC64;

Query Match 76.0%; Score 1426; DB 2; Length 466;
Best Local Similarity 60.4%; Pred. No. 2.2e-94;
Matches 282; Conservative 30; Mismatches 41; Indels 114; Gaps 3;

QY 1 MGSLILLFLAVATRVLSQVLQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60
Db 1 MEFLSWVFLVAILKGVCQVQLVSGGGLVQPGSLTLSCAASGLTVSSNVMHWVRQAP 60
QY 61 GQRLWIGYFSPGNDPFKYNRFGKATLTADTSASTAYVELSLRSEDATVYFCTRS-- 118
Db 61 GKGLEWVSVLYIGGARY-YADSVKGRFTISRDNKNTLYLQMSLRAREDATVYCARNGY 119
QY 119 -LNMAVGGQTLTVTSASSTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNS 177
Db 120 VTPAAWGGQTLTVTSASSTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNS 179
QY 178 GALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVPKSC 237
Db 180 GALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVPKSC 239
QY 238 DKTHTCPPCP----- 247
Db 240 DKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYD 299
QY 248 ----- 247
Db 300 GVEVHNAKTPREEQYNSTRYVSVLTVLHQDLNGKEYKCKVSNKALPAPIETKISKAK 359
QY 248 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 307
Db 360 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 419
QY 308 DGSFFLYSKLTVDKSRWQQGNVSCFVSIMHEALHNHYTQKSLSLSPGK 354
Db 420 DGSFFLYSKLTVDKSRWQQGNVSCFVSIMHEALHNHYTQKSLSLSPGK 466

RESULT 11
Q6FJA4 HUMAN
ID Q6FJA4 HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6FJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]

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Db 1 MERGLSVFLVAILKGVQCEVQLVQSGGLVQPGSLKLSAASGETVNNYVWHRVRQAP 60
QY 61 GORLEWIGYFSPGNDPKYNERFKGKATLTADTSASTAYVELSLSRSEDATVYFCTRS-- 118
Db 61 GKGLVWVSLNRDASSETAYAEFVQGRFTISRDNKNTLFLQLSLRAEDATVYICARGF 120
QY 119 LNMYAGQGLTIVTSSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYPPPEPVTVSNNSG 178
Db 121 GNFDMQGGTLVTVSSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYPPPEPVTVSNNSG 180
QY 179 ALTSVGHVTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKEPKSCD 238
Db 181 ALTSVGHVTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKEPKSCD 240
QY 239 KHTTCCPPCP----- 247
Db 241 KHTTCCPPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 300
QY 248 -----G 248
Db 301 VEHNNAKTPREBQYNSTYRVWSVLTVLHQDLWNGKEYKCRVSNKALPAPIEKTISKAKG 360
QY 249 QPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIATAVESNGQPNKYKTTTPVLDS 308
Db 361 QPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIATAVESNGQPNKYKTTTPVLDS 420
QY 309 GSFFLYSKLTVDKSRWQOQNVFSCSVNHEALHNHYTQKSLSLSPGK 354
Db 421 GSFFLYSKLTVDKSRWQOQNVFSCSVNHEALHNHYTQKSLSLSPGK 466

RESULT 14
Q5RE17_PONPY
ID Q5RE17_PONPY PRELIMINARY; PRT; 475 AA.
AC Q5RE17_2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKF2p469C2335.
GN Name=DKF2p469C2335;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Kidney;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Oanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; CB857722; CH89990.1; -, mRNA.
DR SNR; Q5RE17_21-475.
DR GO; GO:0030106; F.MHC class I receptor activity; IEA.
DR GO; GO:0019883; P-antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P-antigen processing, endogenous antigen via . . . ; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51898 MW; 04BDBE096A2CD529 CRC64;
```

Query Match

75.2%; Score 1411.5; DB 2; Length 475;

```
Best Local Similarity 58.6%; Pred. No. 2.5e-93;
Matches 279; Conservative 32; Mismatches 42; Indels 123; Gaps 3;
QY 1 MGWLLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGVTFTDHAITHWVKQNP 60
Db 1 MGFVSLALLAVLQACADIQLVQSGAEVKRFGESLRISCKSGVTFTDHWLGWRQMP 60
QY 61 GORLEWIGYFSPGNDPKYNERFKGKATLTADTSASTAYVELSLSRSEDATVYFCTRSLN 120
Db 61 GKGLMLGMIDPSNSGTYKYNRSPEGHTTISADMSISTAYLQMTSLKASDAIYCAR-LR 119
QY 121 MA-----YNGOGLTIVTSSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYFP 168
Db 120 LSGTNSYHKRSYFQFGQGLTVLTVSLASTKGPVFPPLAPSSRSTSGGTAALGCLVKDYFP 179
QY 169 EPTVSWNSGALTSVGHVTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKV 228
Db 180 EPTVSWNSGALTSVGHVTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKV 239
QY 229 DKVBPSPKCDKHTCCPPCP----- 247
Db 240 DKVBPSPKCDTTPRCPCCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDP 299
QY 248 ----- 247
Db 300 EVKFNWYVDGEVHNNAKTPREBQYNSTYRVWSVLAVVHQDLWNGKEYKCKVSNKALPAP 359
QY 248 -----GPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIATAVESNGQPNKY 298
Db 360 IEKTISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIATAVESNGQPNKY 419
QY 299 KTTTPVLDSGGSFFLYSKLTVDKSRWQOQNVFSCSVNHEALHNHYTQKSLSLSPGK 354
Db 420 KTTTPVLDSGGSFFLYSKLTVDKSRWQOQNVFSCSVNHEALHNHYTQKSLSLSPGK 475

RESULT 15
Q6PI81_HUMAN
ID Q6PI81_HUMAN PRELIMINARY; PRT; 478 AA.
AC Q6PI81;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McQuellan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
```

```

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) .
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC041037; AHA41037.1; -, mRNA.
DR HSSP; P01861; IADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PSS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 478 AA; 52667 MW; 17BED38D917970D6 CRC64;

Query Match 75.2%; Score 1410; DB 2; Length 478;
Best Local Similarity 57.7%; Pred. No. 3.2e-93;
Matches 276; Conservative 34; Mismatches 44; Indels 124; Gaps 2;

QY 1 MGWSLILLFLVAVATRVLSQVLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1 MELGLSWFLVAILEGVQCEVLVQSGGLVQPGSLRLSCAASGFTFSYMSWYRQAP 60

QY 61 GORLEWIGYFSPGNDPFKYNERFKGKATLTADTSASTAYVELSSLRSEDTAVYFCTRSLN 120
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
61 GKGLEWVANIQDGSSEKYVDSVKGRTTISRDNAGNSLYLQMSLRREDIATVYICAREFE 120

QY 121 -----MAYWQGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 166
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
121 STMTTNADYYFYMDVMVGKGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180

QY 167 FPEPVTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTTQTYICNVNHKPSNT 226
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
181 FPEPVTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTTQTYICNVNHKPSNT 240

QY 227 KVDKKVPEKSCDKHTCPCPCP----- 247
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
241 KVDKRVPEKSCDKHTCPCPCAPPELLGGPSVFLFPPPKDITLMISTRPEVTCVVVDVSH 300

QY 248 ----- 247
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
301 DPEVKFNWYVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360

QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGOPEN 296
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
361 APIETKISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEHESNGOPEN 420

QY 297 NYKTTPPVLDSDGGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
421 NYKTTPPVLDSDGGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478
```

Search completed: February 16, 2006, 10:22:53  
Job time : 186.96 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1127.5	60.1	469	2	S37483	Ig gamma-2a chain C
2	1116	59.5	330	1	GHRU	Ig gamma-1 chain C
3	1094	58.3	446	2	S40295	Ig gamma-2a chain
4	1066	56.8	474	1	G2NS11	Ig gamma-2b chain
5	1030.5	54.9	475	2	S01321	Ig gamma-2b chain
6	1006	53.6	326	1	G2HRU	Ig gamma-2 chain C
7	997.5	53.2	377	2	A23511	Ig gamma-3 chain C
8	995.5	53.1	377	2	A60764	Ig gamma-3 chain C
9	981.5	52.3	444	2	PC34436	monoclonal antibod
10	974.5	51.9	327	1	G4HRU	Ig gamma-4 chain C
11	946	50.4	470	2	S22080	Ig heavy chain pre
12	940	50.1	472	2	S31459	Ig gamma-1 chain -
13	852	45.4	374	2	S69339	Ig heavy chain V r
14	814.5	43.4	241	2	S68131	Ig heavy chain (DO
15	809	43.1	246	2	S38950	Ig gamma chain m
16	803.5	42.8	249	2	S65340	Ig heavy chain VHI
17	777	41.4	220	2	A49444	Ig gamma-1 heavy c
18	769	41.0	548	2	S38864	Ig epsilon chain C
19	748	39.9	218	2	A36040	Ig heavy chain V-I
20	737	39.3	328	2	I47159	Ig gamma 2a chain
21	733	39.1	328	2	I47158	Ig gamma 1 chain c
22	732	39.0	328	2	I47161	Ig gamma 3 chain c
23	731	39.0	328	2	I47160	Ig gamma 2b chain
24	726	38.7	214	2	FC4202	monoclonal antibod
25	722.5	38.5	323	1	GHRB	Ig gamma chain C r
26	722	38.5	322	2	PS0019	Ig gamma-2a chain
27	720	38.4	326	2	PS0017	Ig gamma-1 chain C
28	715.5	38.1	221	2	S49220	Ig gamma-1 chain -
29	707	37.7	549	2	S04845	Ig heavy chain pre

Db 419 VLSDSGSYFMYSLRVEKQWVNRNSYSVVEGLNHHHTTKSFRTPGK 469

RESULT 2

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004

C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370

A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,

A:Note: Lys-330 is removed after translation

R:Harris, L.J.

Submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAB>

A:Cross-references: UNIPARC:UPI000013C6FE; EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-1137235-330 <TAK>

A:Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96, 'R', '98-135 <CUN>

A:Cross-references: UNIPARC:UPI000017378D

A:Note: this sequence has the G1m(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154, 'Q', '156-165, 'Q', '167-176, 'Q', '178-194, 'N', '196-197, 'D', '199-238, 'E', '240,

A:Cross-references: UNIPARC:UPI000017378E

A:Note: this sequence has the G1m(17) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

igen Primaerstruktur.

A:Reference number: A91668; MUID:77070269; PMID:826475

A:Contents: myeloma protein Nie

A:Accession: B91668

A:Molecule type: protein

A:Residues: 1-34, 'Q', '36-96, 'K', '98-115, 'Q', '117-197, 'D', '199-238, 'D', '240, 'L', '242-268, 'E', '27

A:Cross-references: UNIPARC:UPI000017378F

A:Note: this sequence has the G1m(17) and G1m(1) markers

R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983

A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOI

A:Reference number: A91723; MUID:83289131; PMID:6884994

A:Contents: myeloma protein KOI; disulfide bonds

A:Accession: A91723

A:Molecule type: protein

A:Residues: 1-96, 'R', '98-197, 'D', '199-238, 'E', '240, 'M', '242-266, 'D', '268-271, 'D', '273-330 <SCH

A:Cross-references: UNIPARC:UPI0000173790

A:Note: this sequence has the G1m(3) and G1m(non-1) markers

R:Gall, W.E.; Edelman, G.M.

Biochemistry 9, 3188-3196, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid

A:Reference number: A90565; MUID:71064027; PMID:4923144

A:Contents: annotation; disulfide bonds

R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976

A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob

enonide cleavage products, and the disulfide bridges.

A:Reference number: A91667; MUID:77070267; PMID:1002129

A:Contents: annotation; disulfide bonds

C:Genetics:

A:Gene: GDB:IGHG1

A:Cross-references: GDB:120085; OMIM:147100

A:Map position: 14q32.33-14q32.33

A:Introns: 9/1; 114/1; 224/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:137-206/Domain: immunoglobulin homology <IM2>

F:243-310/Domain: immunoglobulin homology <IM3>

F:27-93,144-204,250-308/Disulfide bonds: #status experimental

F:103/Disulfide bonds: interchain (to light chain) #status experimental

F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental

F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 59.5%; Score 1116; DB 1; Length 330;

Best Local Similarity 66.7%; Pred. No. 1.4e-60;

Matches 220; Conservative 0; Mismatches 0; Indels 110; Gaps 1;

QY 135 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKGYFPEPVTVSMNSGALTSGVHTFPAVLQSS 194

Db 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKGYFPEPVTVSMNSGALTSGVHTFPAVLQSS 60

QY 195 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPPCP----- 247

Db 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPPCPELLOG 120

QY 248 ----- 247

Db 121 PSVFLFPKPCKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

QY 248 -----GQPREPQVYTLPPSRDE 264

Db 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPVYTLPPSRDE 240

QY 265 LTKNQVSLTCLVKGYFSDIAVEVESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 324

Db 241 LTKNQVSLTCLVKGYFSDIAVEVESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300

QY 325 QGQNVFSCSVMEALHNNHYTKSLSPGK 354

Db 301 QGQNVFSCSVMEALHNNHYTKSLSPGK 330

RESULT 3

S40295

Ig gamma-2a chain (mAb735) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Apr-1994 #sequence revision 07-Apr-1994 #text\_change 09-Jul-2004

R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; B

C:Accession: S40295

submitted to the EMBL Data Library, January 1993

A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against

A:Reference number: S40295

A:Accession: S40295

A:Molecule type: protein

A:Residues: 1-446 <KLE>

A:Cross-references: UNIPROT:Q99L25; UNIPARC:UPI0000176F38

C;Genetics:  
A;Map position: 12  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F;1-446/Product: Ig gamma-2a chain protein; immunoglobulin; pyroglutamic acid  
F;1-117/Domain: V-D-J region <VDJ>  
F;118-446/Domain: C region <CHR>  
F;118-214/Domain: C1 region <CH1>  
F;231-340/Domain: C2 region <CH2>  
F;341-446/Domain: C3 region <CH3>  
F;360-427/Domain: immunoglobulin homology <IMM>  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;22-96,144-199,261-321,367-425/disulfide bonds: #status predicted  
F;132/disulfide bonds: interchain (to light chain) #status predicted  
F;224,227,229/disulfide bonds: interchain #status predicted  
F;297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 58.3%; Score 1094; DB 2; Length 446;  
Best Local Similarity 48.9%; Pred. No. 4e-59;  
Matches 219; Conservative 41; Mismatches 72; Indels 116; Gaps 4;

QY 20 QVQLQSGGELVLRPGASVKISCKASGYTFDTHAIHWKONPGORLEWIGYFSPGNDPKY 79  
Db 1 QIQLQSGGELVLRPGASVKISCKASGYTFDTHAIHWKONPGORLEWIGYFSPGNDTKY 60

QY 80 NERFKGKATLTADTSASTAYVELSLRSDTAVYFCTR--SLMAYWGQGLTVTVSSAST 137  
Db 61 NEKFKGKATLTVDTSSTAYMQLSLTSEDSAVYFCARGGKPMYWGQGSTVTVSSAKT 120

QY 138 KGPSVPPLAPSSKSTSGGTAALGCLVKDYPPPPVTVSNAGLTSGVHTFPFVAVLQSGLY 197  
Db 121 TAPSVYPLAPVCGDITGSSVTLGCLVKGYFPEPEPTLTWNSGSLSSGVHTFPFVAVLQSD-LY 179

QY 198 SLSVVTVPSSSLGTQTYICNVNKPSTNVKDKVPKSCDKTHTCPPC----- 246  
Db 180 TLSSSVTVTSSTWPSQSITCNVAHPASTTKVDKIEPRG-PTKPCPPCKCAPNLLGGP 238

QY 247 ----- 246

Db 239 SVFIFFPKIKDVLMLISLPMVTCVVVDSEDDPDVQISWFNVNVETLTATQTHREDYNS 298

QY 247 -----PGQPREPVYTLPPSRDEL 265

Db 299 TLRVVSALPIQHDMWMSGKEFKCKVNNKDLPAPIERTISKPGSVRAPQVYVLPPEBEM 358

QY 266 TKNOVSLTCLVKFGPSDIAVWESNGQPENNYKTPPVLDSDGSFELYSKLTVDKSRWQ 325

Db 359 TRKQVTLTCVTDMPEDIVYEWNTNGKTELNYKTEPVLDSDGSYFMYSKURVEKQNV 418

QY 326 QGNVFCSCVMEALHNHYTQKSLSLSPG 353  
Db 419 ERNSYSCSVVHEGLHNHHTTKFSRTPG 446

RESULT 4  
G2MS11  
Ig gamma-2b chain - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1980 #sequence\_revision 01-Dec-2000 #text change 09-Jul-2004  
C;Accession: S25057; A02157; A26232; A26233; A53598  
R;Fischer, R.; Voss, A.; Nierbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
submitted to the EMBL Data Library, July 1992  
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m  
A;Reference number: S25057  
A;Accession: S25057  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-474 <FIS>  
A;Cross-references: UNIPROT:P01866; UNIPARC:UPI0000116095; EMBL:X67210; NID:954826; PIDN  
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.  
Nature 289, 786-789, 1990  
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from n

A;Reference number: A02157; MUID:80120716; PMID:6766534  
A;Contents: a allele  
A;Accession: A02157  
A;Molecule type: DNA  
A;Residues: 138-161, 'L', 163-189, 'FP', 193-474 <VAM>  
A;Cross-references: UNIPARC:UPI00000272D2; GB:J00461  
A;Note: the sequence was determined from the germline gene  
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.  
Science 206, 1299-1303, 1979  
A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b he.  
A;Reference number: A26235; MUID:80081501; PMID:117548  
A;Contents: MPC 11  
A;Accession: A26235  
A;Molecule type: mRNA  
A;Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU1>  
A;Cross-references: UNIPARC:UPI00001737AF  
A;Note: Lys-474 is probably removed posttranslationally  
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
Science 206, 1303-1306, 1979  
A;Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob.  
A;Reference number: A26232; MUID:80081502; PMID:117549  
A;Accession: A26232  
A;Molecule type: DNA  
A;Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>  
A;Cross-references: UNIPARC:UPI00001737AF  
R;Ollo, R.; Rougeon, F.  
Nature 296, 761-763, 1982  
A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma  
A;Reference number: A26233; MUID:82173203; PMID:6803173  
A;Contents: b allele  
A;Accession: A26233  
A;Molecule type: DNA  
A;Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>  
A;Cross-references: UNIPARC:UPI00001737B0; GB:J00461  
R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Mateunaga, C.; Yamamoto, K.; Irimura, T.; Takahagi  
J. Biol. Chem. 269, 12345-12350, 1994  
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
A;Reference number: A53598; MUID:94216359; PMID:7512967  
A;Accession: A53598  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 234-251 <KIM>  
A;Cross-references: UNIPARC:UPI00001737B1  
C;Comment: The a allele sequence is shown.  
C;Genetics:  
A;Introns: 138/1; 236/1; 258/1; 368/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1.  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob  
F;157-222/Domain: immunoglobulin homology <IMI>  
F;236-257/Region: hinge  
F;281-350/Domain: immunoglobulin homology <IM2>  
F;387-454/Domain: immunoglobulin homology <IM3>  
F;152/disulfide bonds: interchain (co light chain) #status predicted  
F;164-220,288-348,394-452/disulfide bonds: #status predicted  
F;247,250,253,256/disulfide bonds: interchain (to heavy chain) #status predicted  
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.8%; Score 1066; DB 1; Length 474;  
Best Local Similarity 45.6%; Pred. No. 2.1e-57;  
Matches 216; Conservative 49; Mismatches 89; Indels 120; Gaps 4;

QY 1 MGWSLILFLVAVATRVLSQVQLVSGAEVWVPGASVKISCKASGYTFDTHAIHWKQNP 60  
Db 1 MEWSWIFLFLSGTAGVHSEVQLQSGPELVNPGASVKISCKASGYTFITYVHWVKQKP 60

QY 61 GQRLWIGYFSPGNDPKYNERFKGKATLTADTSASTAYVELSLRSDTAVYFCTRSLN 120  
Db 61 GQGLWIGVYNPKDGTKEFKGKATLT3DKSNNTAYMELSSLTSEDSAVVYCARDYD 120

QY 121 ---MAYWGQGLTVTVSSASTKPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSN 177

Db 121 YDFAWYGQGLTVTVSAAKTTTPSYVYPLAPGCGDTTSSVTSGLVKGYFPESVTVTWNS 180  
QY 178 GALTSGVHTFPVAVLQSSGLYSLSSVVTVPPSSLSGTQTYICNVNHPKSNTKVDKVEPKS- 236  
Db 181 GSLSSSVHTLSQALLQSGLYTMSSSVTVPSSTWPSQTVCVAHPASSTVTDKLEPSPG 240  
QY 237 -----CDKTHTCP----- 244  
Db 241 ISTINPCPPCKECHKCPAPNLEGGSPVFIFPPNPKDVLMSLTPKTCVVVDVSDDDPDV 300  
QY 245 -----PCP-- 247  
Db 301 QISWFWNVVEVHTAQQTQTHREDYNSIRVSVTLPIQHQQDMWSGKRFCKVNNKDLPSPT 360  
QY 248 -----GQPRPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNQPNPNTK 300  
Db 361 RTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVGFNPGDISVEMTSNGHTEENYKD 420  
QY 301 TTPVLDSGGSFELYSLKLTVDKSRWQGNVPSCSVMHEALHNHYTKLSLSLSPGK 354  
Db 421 TAPVLDSGGSFYISKLNMTSKWEKTDSCNVRHEGLKNYLTKTISRSPGK 474  
  
RESULT 5  
S01321  
Ig gamma-2b chain precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 23-Jul-1999  
C:Accession: S01321  
Eur. J. Biochem. 176, 287-295, 1988  
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a  
A:Reference number: S01320; MUID:88329081; PMID:3138116  
A:Accession: S01321  
A:Molecule type: mRNA  
A:Residues: 1-475 <EL>  
A:Cross-references: UNIPARC:UPI0000115DDB; EMBL:X13188; NID:G51780; PIDN:CAA31580.1; PID  
A>Note: this sequence was determined from the differentiated gene  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>  
F:159-223/Domain: immunoglobulin homology <IMM>  
  
Query Match 54.9%; Score 1030.5; DB 2; Length 475;  
Best Local Similarity 45.0%; Pred. No. 3e-55;  
Matches 214; Conservative 47; Mismatches 92; Indels 123; Gaps 5;  
  
QY 1 MGWSLTLFLVAVATRVLSQVQLVQSGAEVVRPGASVKISCKASGYTFDTHAIHWKQNP 60  
Db 1 MEWIFILFSLGTAGVQSQVQLQSGAEIARPGASVKLSCKASGYTLTSYGLISWVKQT 60  
  
QY 61 GQRLIEWIGFSPGNDPFKYNRFGKATLTADTSATYVELLSRSEDTAVYFCFTR-- 118  
Db 61 GQGLEWIGEIPGSGNSYFNKFGKATLTVDKSSSTAYVHLSSLTSEDSAVYFCAGPRQ 120  
  
QY 119 ----LNMAYGQGTLTVTSASASTKPSVFPPLAPSKTSGGTAALGCLVKDYDPEPPTVSW 175  
Db 121 VGLLPPGYMGQGLTVTASAAKTTTPSYVYPLAPGCGDTTSSVTLGCLVKGYFPESVTVTW 180  
  
QY 176 NSGALTSGVHTFPVAVLQSSGLYSLSSVVTVPPSSLSGTQTYICNVNHPKSNTKVDKVEPK 235  
Db 181 NSGSLSSSVHTFPALLIQ-SGLYTMSSSVTVPPSSVQTVTCVAHPASSTVTDKLEPS 239  
  
QY 236 S-----CDKTHTCP----- 244  
Db 240 GPTSTINPCPPCKECHKCPAPNLEGGSPVFIFPPNPKDVLMSLTPKTCVVVDVSDDDP 299  
QY 245 -----PCP 247  
Db 300 DVQISWFWNVVEVHTAQQTQTHREDYNSIRVSVTLPIQHQQDMWSGKRFCKVNNKDLPPAP 359  
QY 248 -----GQPRPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNQPNPNTK 298

Db 360 IERTISKIKGIVRAPQVYILSPPEQLSRKDVSLTCLAVGSPEDISVEMTSNGHTEENY 419  
QY 299 KTTTPVLDSGGSFELYSLKLTVDKSRWQGNVPSCSVMHEALHNHYTKLSLSLSPGK 354  
Db 420 KDTAPVLDSGGSFYISKLNMTSKWEKTDSCNVRHEGLKNYLTKTISRSPGK 475  
  
RESULT 6  
G2HU  
Ig gamma-2 chain C region - human  
C:Species: Homo sapiens (man)  
C>Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 09-Jul-2004  
C:Accession: A93906; A92809; A90752; A93132; A02148  
R:Ellison, J.; Hood, L.; U.S.A. 79, 1984-1988, 1982  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con  
A:Reference number: A93906; MUID:82197621; PMID:6804948  
A:Accession: A93906  
A:Molecule type: DNA  
A:Residues: 1-326 <EL>  
A:Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00230; NID:G32  
A>Note: Lys-326 is probably removed posttranslationally  
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f  
A:Reference number: A92809; MUID:81007873; PMID:6774012  
A:Contents: myeloma protein Til  
A:Accession: A92809  
A:Molecule type: protein  
A:Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>  
A:Cross-references: UNIPARC:UPI0000173791  
A>Note: Trp156 is at or near the complement-binding site  
R:Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A:Title: The amino acid sequences of the three heavy chain constant region domains of a  
A:Reference number: A90752; MUID:80001357; PMID:113060  
A:Contents: myeloma protein Zie  
A:Accession: A90752  
A:Molecule type: protein  
A:Residues: 1-24,'E',26-57,'BV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-  
A:Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793  
A>Note: this sequence has since been revised  
R:Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin  
A:Reference number: A93132; MUID:80114419; PMID:118920  
A:Contents: Zie  
A:Accession: A93132  
A:Molecule type: protein  
A:Residues: 238-275 <HOF>  
A:Cross-references: UNIPARC:UPI0000173794  
R:Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A:Reference number: A94591  
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A>Note: the revised sequence differs from that shown in having 60-Ala and in the amidat  
ned  
R:Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.  
A:Reference number: A90253; MUID:72033500; PMID:4940472  
A:Contents: annotation; myeloma protein Sa, disulfide bonds  
R:Frangione, B.; Milstein, C.; Fink, J.R.L.  
Nature 221, 145-148, 1969  
A:Title: Structural studies of immunoglobulin G.  
A:Reference number: A93157; MUID:69064124; PMID:5782707  
A:Contents: annotation; Sa, disulfide bonds  
C:Genetics:  
A:Gene: GDB:ICHS2  
A:Cross-references: GDB:119338; OMIM:147110  
A:Map position: 14q32.33-14q32.33  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kaf

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: Immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:133-202/Domain: immunoglobulin homology <IM2>  
F:239-306/Domain: immunoglobulin homology <IM3>  
F:14/bisulfide bonds: interchain (to light chain) #status experimental  
F:27-83,140-200,246-304/Disulfide bonds: #status experimental  
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:176/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match : 53.6%; Score 1006; DB 1; Length 326;  
Best Local Similarity: 61.1%; Pred. No. 6e-54; Indels 112; Gaps 2;  
Matches 201; Conservative 7; Mismatches 9;

QY 135 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 194  
DB 1 ASTKGPSVFLPAPCSRSTESSTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 60

QY 195 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVPKSCDKHTTCCPPC----- 247  
DB 61 GLYSLSVVTVPSNFGTQTYTCNVDHKPSNTKVDKTKVERKCCVE---CPPCPAPPVAGP 117

QY 248 ----- 247

DB 118 SVFLFPKPQDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQFNS 177

QY 248 -----GOPREPQVYTLPPSRDEL 265

DB 178 TRVVSVLTVVHQDLNGKEYCKVSKNKGLPAPIEKTIKTKGQPREPQVYTLPPSRDEM 237

QY 266 TKNQVSLTCLVGFYPSDIAVWESNGQPNNTKTPPVLDSDGSFFLYSKLTVDKSRWQ 325  
DB 238 TKNQVSLTCLVGFYPSDIAVWESNGQPNNTKTPPVLDSDGSFFLYSKLTVDKSRWQ 297

QY 326 QGNVFCSCVMHEALHNHYTKLSLSPGK 354  
DB 298 QGNVFCSCVMHEALHNHYTKLSLSPGK 326

RESULT 7

A23511

Ig gamma-3 chain C region (allotype G3m(b)) - human  
C:Species: Homo sapiens (man)  
C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
C:Accession: A23511  
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
Nucleic Acids Res. 14, 1779-1789, 1986  
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c  
A:Reference number: A23511; MUID:86148507; PMID:3081877  
A:Accession: A23511  
A:Molecule type: DNA  
A:Residues: 1-377 <HUC>  
A:Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:g33070; PIDN:CAA272  
C:Genetics:  
A:Gene: GDB:IGHG3  
A:Cross-references: GDB:119339; OMIM:147120  
A:Map position: 14q32.33-14q32.33  
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:20-85/Domain: immunoglobulin homology <IM>

Query Match : 53.2%; Score 997.5; DB 2; Length 377;  
Best Local Similarity: 53.8%; Pred. No. 2.3e-53; Indels 157; Gaps 2;  
Matches 203; Conservative 8; Mismatches 9;

QY 135 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 194  
DB 1 ASTKGPSVFLPAPCSRSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 60

QY 195 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV----- 232

DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVELKTPLGDTTHTCPRCPKSC 120

QY 233 -----EPKSCDKTHTCCPPC----- 247

DB 121 DTPPCPCPCPKSCDTPPPCPCPKSCDTPPPCPCPAPELLGGPSVFLFPPKPKDT 180

QY 248 ----- 247

DB 181 LMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQNSTFRVVSULTVLH 240

QY 248 -----GOPREPQVYTLPPSRDELTKNOVSLTCLVK 277

DB 241 QDLNGKEYCKVSKNKAUAPAPIEKTIKTKGQPREPQVYTLPPSRDEMTKNQVSLTCLVK 300

QY 278 GYPSDIAVWESNGQPNNTKTPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHE 337

DB 301 GYPSDIAVWESNGQPNNTKTPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHE 360

QY 338 ALHNHYTKLSLSPGK 354  
DB 361 ALHNRTQKLSLSPGK 377

Db 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVELKTPLGDTTHTCPRCPKSC 120

QY 233 -----EPKSCDKTHTCCPPC----- 247

Db 121 DTPPCPCPCPKSCDTPPPCPCPKSCDTPPPCPCPAPELLGGPSVFLFPPKPKDT 180

QY 248 ----- 247

Db 181 LMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQNSTFRVVSULTVLH 240

QY 248 -----GOPREPQVYTLPPSRDELTKNOVSLTCLVK 277

Db 241 QDLNGKEYCKVSKNKAUAPAPIEKTIKTKGQPREPQVYTLPPSRDEMTKNQVSLTCLVK 300

QY 278 GYPSDIAVWESNGQPNNTKTPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHE 337

Db 301 GYPSDIAVWESNGQPNNTKTPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHE 360

QY 338 ALHNHYTKLSLSPGK 354

Db 361 ALHNRTQKLSLSPGK 377

RESULT 8

A60764

Ig gamma-3 chain C region, form LAT - human  
C:Species: Homo sapiens (man)  
C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 31-Dec-2004  
C:Accession: A60764  
R:Huck, S.; Lefranc, G.; Lefranc, M.P.  
Immunogenetics 30, 250-257, 1989  
A:Title: A human immunoglobulin IGHC3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conver  
A:Reference number: A60764; MUID:90007613; PMID:2571587  
A:Accession: A60764  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-377 <HUC>  
A:Cross-references: UNIPROT:Q8N4Y9; UNIPARC:UPI0000176F0B  
C:Superfamily: immunoglobulin homology  
C:Keywords: immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM>

Query Match : 53.1%; Score 995.5; DB 2; Length 377;  
Best Local Similarity: 53.8%; Pred. No. 3e-53; Indels 157; Gaps 2;  
Matches 203; Conservative 8; Mismatches 9;

QY 135 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 194  
DB 1 ASTKGPSVFLPAPCSRSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 60

QY 195 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV----- 232

Db 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVELKTPLGDTTHTCPRCPKSC 120

QY 233 -----EPKSCDKTHTCCPPC----- 247

Db 121 DTPPCPCPCPKSCDTPPPCPCPKSCDTPPPCPCPAPELLGGPSVFLFPPKPKDT 180

QY 248 ----- 247

Db 181 LMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQNSTFRVVSULTVLH 240

QY 248 -----GOPREPQVYTLPPSRDELTKNOVSLTCLVK 277

Db 241 QDLNGKEYCKVSKNKAUAPAPIEKTIKTKGQPREPQVYTLPPSRDEMTKNQVSLTCLVK 300

QY 278 GYPSDIAVWESNGQPNNTKTPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHE 337

Db 301 GYPSDIAVWESNGQPNNTKTPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHE 360

QY 338 ALHNHYTKLSLSPGK 354

Db 361 ALHNRTQKLSLSPGK 377



RESULT 9  
PC4436  
monoclonal antibody 13-1 heavy chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jan-2000  
A:Accession: PC4436  
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.  
Biochem. Biophys. Res. Commun. 240, 566-572, 1997  
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin  
A:Reference number: JCS810; MUID:98063277; PMID:9398605  
A:Accession: PC4436  
A:Molecule type: protein  
A:Residues: 1-444 <AKA>  
A:CROSS-references: UNIPARC:UPI0000176F41  
C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed against  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:251-320/Domain: immunoglobulin homology <IMM>  
F:22/Disulfide bonds: interchain (to 98) #status predicted  
F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 52.3%; Score 981.5; DB 2; Length 444;  
Best Local Similarity 41.9%; Pred. No. 2.5e-52;  
Matches 188; Conservative 66; Mismatches 76; Indels 119; Gaps 5;

QY 20 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNPQORLEWIGYFSPGNDP-- 77  
DB 1 EVQVETGGGLVRPGNSLKSLCSTGFTFSNRMHWLRQPPGKRLIEWIAIVTKSDNYGA 60

QY 78 KNERFKGKATLTADTSASTAVELSLSEDTAVYFCTRS---LNMYWGQGLTVVSS 134  
DB 61 KYAESVRGRTISRDDSKSVLYQMRLREEDTATYICCTPWVYAMDCMGQGSTIVSS 120

QY 135 ASTKPSVPLAPSSKSTSGGTAALGCLVKDYPPEPTVSNWNSGALTSVHTFPVAVLQSS 194  
DB 121 AKTPPSVPLAPGSAQNSWTLGCLVKGFPEPTVSNWNSGSLSSGVHTFPVAVLQSD 180

QY 195 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPPC----- 246  
DB 181 -LYTLSSVTVPPSSSTWPSSETVTCNVAHPASSTKVDKVIIPRDG---CKPCICTVPEVS 235

QY 247 ----- 246

DB 236 SVFIIPPCKDVLITITPKVTCVVVDISKDDPEVQFSWFDVDDVEVHTAQTQPREEQFNS 295

QY 247 -----PQPREQVTVTLPPSRDEL 265  
DB 296 TFRSVSELPIMHQDWLNGKEFKCRVNSAAPPAPIEKTISKTKGRPKAPQVYTIIPPKEQM 355

QY 266 TRNQVSLTCLVKGFPSDIAVESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 325  
DB 356 AKDKVSLTCMTDFPEDITVEMQWQPAENYKNTQIMDTDGSYFVYSLKNVQKSNWE 415

QY 326 QGNVFCSCVMHEALHNHYTKSLSPGK 354  
DB 416 AGNTFTCSVLHEGLHNHTEKSLSPGK 444

RESULT 10  
GHU  
Ig gamma-4 chain C region - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004  
A:Accession: A90933; A90249; A02150  
R:Ellison, J.; Buxbaum, J.; Hood, L.  
DNA 1, 11-18, 1991  
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
A:Reference number: A90933; MUID:83157104; PMID:6299662  
A:Accession: A90933  
A:Molecule type: DNA  
A:Residues: 1-327 <ELL>  
A:CROSS-references: UNIPROT:P01861; UNIPARC:UPI0000047190

A:Note: the sequence was determined from the germline gene  
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
Biochem. J. 117, 33-47, 1970  
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant  
A:Reference number: A90249; MUID:70207560; PMID:4192699  
A:Accession: A90249  
A:Molecule type: protein  
A:Residues: 1-30; 81-326 <PIN>  
A:CROSS-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796  
C:Genetics:  
A:Gene: GDB:IGHG4  
A:CROSS-references: 14G32.33-14G32.33  
A:Map position: 99/1; 111/1; 221/1  
A:Introns: 99/1; 111/1; 221/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)  
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:99-110/Region: hinge  
F:134-203/Domain: immunoglobulin homology <IM2>  
F:240-307/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,141-201,247-305/Disulfide bonds: #status predicted  
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.9%; Score 974.5; DB 1; Length 327;  
Best Local Similarity 59.7%; Pred. No. 4.8e-52;  
Matches 197; Conservative 9; Mismatches 11; Indels 113; Gaps 2;

QY 135 ASTKPSVPLAPSSKSTSGGTAALGCLVKDYPPEPTVSNWNSGALTSVHTFPVAVLQSS 194  
DB 1 ASTKPSVPLAPSSKSTSGGTAALGCLVKDYPPEPTVSNWNSGALTSVHTFPVAVLQSS 60

QY 195 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPPC----- 247  
DB 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPPC----- 117

QY 248 ----- 247

DB 118 PSVFLPPKPKDMLISRTPEVTVVVDVDSQBDPEVQFNWYVDGVVHNAKTKPREEQFN 177

QY 248 -----GOPREQVTVTLPPSRDE 264  
DB 178 STYRVSVLTVLHQDWLNGKEYKCKVKNKGLPSSIEKTKAKGQPREQVTVTLPPSQEE 237

QY 265 LTKNQVSLTCLVKGFPSDIAVESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 324  
DB 238 MTNQVSLTCLVKGFPSDIAVESNGQPENNYKTTTPVLDSDGSPFLYSRLTVDKSRW 297

QY 325 QGNVFCSCVMHEALHNHYTKSLSPGK 354  
DB 298 QGNVFCSCVMHEALHNHYTKSLSLGK 327

RESULT 11  
S22080  
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine  
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S22080; S06610; A31303  
R:Sanders, P.G.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S22080  
A:Accession: S22080  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-470 <SAN>  
A:CROSS-references: UNIPARC:UPI0000116007; EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:  
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.  
Mol. Immunol. 26, 841-850, 1989



Db 127 YRPSHWGGTLVTVSSPEKSCDKTHTCCPCAPPELLGGPSVFLPPKPKDGLMISRTPEV 186  
QY 160 GCLVKDYFPEPVTVSMN---SGALSGVHFTFAVLQSSGLYSLSSVTVTPSSS-LGTQTY 215  
Db 187 TCVVDVSHEDPEVKFNMYVDGVEHNAKTKPREEQYNSTYRVSVLTLHQDWLNGKEY 246  
QY 216 ICNVNHHKPSNTKVDKKVPEKSCDKTHTCCPCGQPREPOVYTLPPSRDELTKNOVSLTCL 275  
Db 247 KCKVSNKALPAPIEK-----TISKAKGQPREPOVYTLPPSREEMTKNQVSLTCL 295  
QY 276 VKGFYPSDIAVWESNGQPNENYKTTTPPVLDSDGSFELYSKLTVDKSRWQOQGNVFSQV 335  
Db 296 VKGFYPSDIAVWESNGQPNENYKTTTPPVLDSDGSFELYSKLTVDKSRWQOQGNVFSQV 355  
QY 336 HEALHNHYTKQSLSPGK 354  
Db 356 HEALHNHYTKQSLSPGK 374  
RESULT 14  
S69131  
Ig heavy chain (DOT) - human (fragment)  
N:Alternate names: anti-riboflavin IgG Fd fragment  
C:Species: Homo sapiens (man)  
C:Date: 12-Feb-1998 #sequence\_revision 22-May-1998 #text\_change 21-Jan-2000  
C:Accession: S69131  
R:Stoppini, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Ferri, G.  
Eur. J. Biochem. 228, 886-893, 1995  
A:Title: Characterization of the two unique human anti-flavin monoclonal immunoglobulins  
A:Reference number: S69130; MUID:95255298; PMID:7737190  
A:Accession: S69131  
A:Molecule type: protein  
A:Residues: 1-241 <STO>  
A:Cross-references: UNIPARC:UPI0000176F40  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: blocked amino end; heterotetramer; immunoglobulin; pyroglutamic acid  
F:1-241/Product: Ig heavy chain (DOT) (fragment) #status experimental <MAT>  
F:140-205/Domain: immunoglobulin homology <IMM>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
Query Match 43.4%; Score 814.5; DB 2; Length 241;  
Best Local Similarity 66.8%; Pred. No. 1.6e-42;  
Matches 163; Conservative 23; Mismatches 47; Indels 11; Gaps 4;  
QY 20 QVQLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNPQORLEWIGYFSPGNDDFKY 79  
Db 1 QVQLVQSGVERKVPKGASVRIKSKASGYAFENYIHWVRQAPGLGLEWMGIFNPVAGAVS- 59  
QY 80 NERFKGKATLTADTSASTAYVELSLRSEDVAVYFCTR-----SLNMAVWGOGTLTVTVS 133  
Db 60 SEKFRDLVNSDTSANTVSMQLNRKSDTGRTYFCARVSYDFSQYGMVWGGTIVIS 119  
QY 134 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ 193  
Db 120 SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ 179  
QY 194 SGLYSLSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKKVPEKSCDKTHTCPPCPGQP-RE 252  
Db 180 SGLYSLSVTVTPSSNFGTQTYICNVDHKPSNTKVDKVERKCCVE---CPPCPAPPVAG 236  
QY 253 PQVY 256  
Db 237 PSVF 240  
RESULT 15  
S38950  
Ig gamma chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 19-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Jul-1999  
C:Accession: S38950  
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bi  
Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993

A:Title: Primary structure of the murine monoclonal IGG2a antibody mAb735 against alpha  
A:Reference number: S38950; MUID:94128242; PMID:8297501  
A:Accession: S38950  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-246 <KLE>  
A:Cross-references: UNIPARC:UPI0000176F3B  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:137-201/Domain: immunoglobulin homology <IMM>  
Query Match 43.1%; Score 809; DB 2; Length 246;  
Best Local Similarity 64.4%; Pred. No. 3.6e-42;  
Matches 159; Conservative 28; Mismatches 52; Indels 8; Gaps 4;  
QY 20 QVQLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNPQORLEWIGYFSPGNDDFKY 79  
Db 1 QIQLQSGPELVKPGASVKISKASGYTFDTHAIHWKQNPQORLEWIGYFSPGNDDFKY 60  
QY 80 NERFKGKATLTADTSASTAYVELSLRSEDVAVYFCTR--SLNMAVWGOGTLTVTVSSAST 137  
Db 61 NEKFKGKATLTVDTSSTAYMQLSLTSDSAVYFCARGGKFAVDYWGQGTSTVTVSSAKT 120  
QY 138 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSSGLY 197  
Db 121 TAPSVYPLAPVCGDTTGGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD-LY 179  
QY 198 SLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKKVPEKSCDKTHTCPPC-----PGQPREP 253  
Db 180 TLSSSVTVTSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLLGGP 238  
QY 254 QVYTLPP 260  
Db 239 SVFIPTPP 245  
Search completed: February 16, 2006, 10:23:48  
Job time : 31.798 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 16, 2006, 10:12:02 ; Search time 194.879 Seconds  
(without alignments)  
798.138 Million cell updates/sec

Title: US-10-058-069-7

Perfect score: 1876

Sequence: 1 MGWSILFLVAVATRVLSQ.....MHEALHNHYTKSLSLSPGK 354

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_21.\*

- 1: geneseqp1980s.\*
- 2: geneseqp1990s.\*
- 3: geneseqp2000s.\*
- 4: geneseqp2001s.\*
- 5: geneseqp2002s.\*
- 6: geneseqp2003as.\*
- 7: geneseqp2003bs.\*
- 8: geneseqp2004s.\*
- 9: geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1876	100.0	354	5	Aae27926 Human CH2
2	1876	100.0	354	6	Abb82835 Antibody
3	1770	94.3	347	9	Adw77045 Heavy cha
4	1763.5	94.0	360	9	Adw77049 Heavy cha
5	1762.5	93.9	362	9	Adw77050 Heavy cha
6	1762.5	93.9	603	9	Adw44587 Antibody
7	1762.5	93.9	621	9	Adw44588 Antibody
8	1755.5	93.6	362	9	Adw77053 Heavy cha
9	1683	89.7	360	5	Aae27924 Human CH2
10	1683	89.7	360	6	Abb82833 Antibody
11	1614	86.0	470	5	Aae27923 Human C2B
12	1614	86.0	470	6	Abb82832 Antibody
13	1613.5	86.0	731	4	Aam52156 Humanised
14	1613.5	86.0	741	4	Aam52159 Humanised
15	1613	86.0	470	3	Aab08026 A dimeric
16	1608.5	85.7	729	4	Aam52158 Humanised
17	1608.5	85.7	739	4	Aam52161 Humanised
18	1608	85.7	462	9	Aeb08000 Anti-NOGO
19	1604	85.5	464	8	Adu68011 Mouse ant
20	1603	85.4	470	3	Aaw83036 Anti-Fas
21	1603	85.4	470	3	Aab14776 Humanised
22	1603	85.4	470	3	Aaw90926 Humanised
23	1603	85.4	470	3	Abb74941 Humanised
24	1603	85.4	470	5	Abb74895 Humanised

RESULT 1

AAE27926

ID AAE27926 standard; protein; 354 AA.

XX AAE27926;

AC AAE27926;

XX 27-DEC-2002 (first entry)

XX Human CH2 domain deleted CC49 antibody heavy chain protein.

DE Human CH2 domain deleted CC49 antibody heavy chain protein.

XX Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;

KW neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;

KW non-Hodgkin's lymphoma; haematologic malignancy; tumour;

XX Homo sapiens.

XX WO200260955-A2.

XX 08-AUG-2002.

XX 29-JAN-2002; 2002WO-US002373.

XX 29-JAN-2001; 2001US-0264318P.

XX 16-NOV-2001; 2001US-0331481P.

(IDEC-) IDEC PHARM CORP.

XX BraSlawewy GR, Hanna N, Chinn P;

XX WPI; 2002-698547/75.

XX N-PSDB; AAD45755.

XX Novel domain deleted CC49 antibody reactive with tumor associated antigen -72, or C2B8 antibody reactive with CD20, useful for treating myelosuppressed patient suffering from a neoplastic disorder.

XX Example 2; Fig 4A; 74pp; English.

XX The present invention relates to domain deleted CC49 or C2B8 antibodies. Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain deleted sequence in which CH2 domain has been deleted and are reactive with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive with CD20 and comprise a heavy chain having a sequence of a derived domain deleted C2B8 construct where the CH2 domain has been deleted. Sequences of the invention are useful for imaging a neoplasm. They are also useful for treating myelosuppressed patients suffering from neoplastic disorder such as haematologic neoplasm, preferably non-

CC Hodgkin's lymphoma. Antibodies of the invention are also used to treat  
CC neoplastic disorder, colon cancer and haematologic malignancy. They are  
CC useful for reducing tumour size, inhibiting tumour growth and/or  
CC prolonging the survival time of tumour-bearing animals and for treating  
CC tumours. The present sequence is human CH2 domain deleted CC49 antibody  
CC heavy chain protein. This sequence is used in the exemplification of the  
CC invention  
XX  
SQ Sequence 354 AA;  
Query Match 100.0%; Score 1876; DB 5; Length 354;  
Best Local Similarity 100.0%; Pred. No. 1.2e-114; Indels 0; Gaps 0;  
Matches 354; Conservative 0; Mismatches 0;  
Qy 1 MGWSLILLFLVAVATRVLSQVLQVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQP 60  
Db 1 MGWSLILLFLVAVATRVLSQVLQVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQP 60  
Qy 61 GORLEWIGYFSPGNDDFKYNFRFKGKATLTADTSASTAYVELSLRSEDYAVFCTRSIN 120  
Db 61 GORLEWIGYFSPGNDDFKYNFRFKGKATLTADTSASTAYVELSLRSEDYAVFCTRSIN 120  
Qy 121 MAYWQGTLLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGAL 180  
Db 121 MAYWQGTLLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGAL 180  
Qy 181 TSGVHTFPFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKT 240  
Db 181 TSGVHTFPFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKT 240  
Qy 241 HTCPPCPGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 300  
Db 241 HTCPPCPGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 300  
Qy 301 TTPVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354  
Db 301 TTPVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354  
RESULT 2  
ABB82835  
ID ABB82835 standard; protein; 354 AA.  
XX  
AC ABB82835;  
XX  
DT 31-MAR-2003 (first entry)  
XX  
DE Antibody huCC49 CH2 domain deleted heavy chain.  
XX  
KW CC49; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;  
KW vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotoxic;  
KW thymimetic; hepatotropic; haemostatic; antileprotic; antibacterial;  
KW neuroprotective; antipsoptic; antirheumatic; antiarthritic; antiulcer;  
KW dermatological; immunosuppressive; antiinflammatory.  
XX  
OS Homo sapiens.  
XX  
PN WO200296948-A2.  
XX  
PD 05-DEC-2002.  
XX  
PF 29-JAN-2002; 2002WO-US002374.  
XX  
PR 29-JAN-2001; 2001US-0264318P.  
PR 16-NOV-2001; 2001US-0331481P.  
PR 21-DEC-2001; 2001US-0341858P.  
XX  
PA (IDEC-) IDEC PHARM CORP.  
XX  
PI Braslawsky GR, Hanna N, Chinn P, Hariharan K;  
XX WPI; 2003-140446/13.  
DR N-PSDB; AB224019.  
DR

XX  
PT Novel dimeric antibody useful for treating immune disorder and neoplastic  
PT disorder, has several non-covalently associated monomeric subunits.  
XX  
Example 1; Fig 4A; 78pp; English.  
XX  
CC The invention relates to a dimeric antibody (I) comprising several  
CC monomeric subunits, where the monomeric subunits are non-covalently  
CC associated. (I) is useful for treating a disorder, especially immune  
CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,  
CC resistant Hodgkin's disease high grade, low grade and intermediate grade  
CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),  
CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular  
CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,  
CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic  
CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,  
CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,  
CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small  
CC cleaved and large cell lymphomas, in a mammal (see AB224017 for a  
CC detailed description of the various uses of (I)). The present sequence  
CC represents the antibody huCC49 CH2 domain deleted heavy chain  
XX  
SQ Sequence 354 AA;  
Query Match 100.0%; Score 1876; DB 6; Length 354;  
Best Local Similarity 100.0%; Pred. No. 1.2e-114; Indels 0; Gaps 0;  
Matches 354; Conservative 0; Mismatches 0;  
Qy 1 MGWSLILLFLVAVATRVLSQVLQVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQP 60  
Db 1 MGWSLILLFLVAVATRVLSQVLQVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQP 60  
Qy 61 GORLEWIGYFSPGNDDFKYNFRFKGKATLTADTSASTAYVELSLRSEDYAVFCTRSIN 120  
Db 61 GORLEWIGYFSPGNDDFKYNFRFKGKATLTADTSASTAYVELSLRSEDYAVFCTRSIN 120  
Qy 121 MAYWQGTLLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGAL 180  
Db 121 MAYWQGTLLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGAL 180  
Qy 181 TSGVHTFPFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKT 240  
Db 181 TSGVHTFPFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKT 240  
Qy 241 HTCPPCPGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 300  
Db 241 HTCPPCPGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 300  
Qy 301 TTPVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354  
Db 301 TTPVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354  
RESULT 3  
ADW77045  
ID ADW77045 standard; protein; 347 AA.  
XX  
AC ADW77045;  
XX  
DT 24-MAR-2005 (first entry)  
XX  
DE Heavy chain CH2 domain-deleted huCC49 polypeptide #1.  
XX  
KW Protein production; protein purification; cancer; lymphoma;  
KW autoimmune disease; inflammation; Crohns disease;  
KW inflammatory bowel disease; systemic lupus erythematosus;  
KW ulcerative colitis; rheumatoid arthritis; Goodpasture's syndrome;  
KW Grave's disease; Hashimoto's disease; pemphigus vulgaris;  
KW myasthenia gravis; scleroderma; autoimmune hemolytic anemia;  
KW pernicious anemia; Sjogrens syndrome; immunosuppressive; antianemic;  
KW dermatological; muscular-gen.; neuroprotective; thymimetic;  
KW antithyroid; nephrotoxic; antirheumatic; antiarthritic;  
KW antiinflammatory; antiulcer; gastrointestinal-gen.; neoplasm;

KW immune disorder; huCC49; heavy chain; antibody.  
XX Homo sapiens.  
OS Synthetic.  
XX WO2005000898-A2.  
XX  
XX PD 06-JAN-2005.  
XX  
XX PF 28-JUN-2004; 2004WO-US020944.  
XX  
XX PR 27-JUN-2003; 2003US-0483877P.  
PR 03-OCT-2003; 2003US-0508810P.  
PR 28-OCT-2003; 2003US-0515351P.  
PR 30-OCT-2003; 2003US-0516030P.  
XX  
XX PA (BIOG-) BIOGEN IDEC MA INC.  
XX  
XX PI Braslawsky GR, Glaser S, Yang T, Hopp J, Chinn P;  
XX  
XX DR WPI; 2005-058132/06.  
DR N-PSDB; ADW77043.  
XX  
XX PT New composition comprising polypeptide dimers having at least two binding  
PT sites and at least two polypeptide chains comprising a heavy chain  
PT portion and a synthetic peptide, useful for treating e.g., cancer or  
PT autoimmune diseases.  
XX  
XX PS Disclosure; SEQ ID NO 18; 152pp; English.  
XX  
XX CC The invention relates to a composition comprising polypeptide dimers  
CC having at least two binding sites and at least two polypeptide chains,  
CC where the polypeptide chains comprise at least one heavy chain portion  
CC and a synthetic connecting peptide. The invention also relates to a  
CC nucleic acid molecule comprising a nucleotide sequence encoding a  
CC polypeptide chain, a host cell comprising the nucleic acid molecule, a  
CC connecting peptide, a domain deleted antibody molecule, an antibody  
CC molecule, a method of separating a first properly folded antibody  
CC molecule from a second improperly folded antibody molecule, where each of  
CC the first and second antibody molecules comprises four polypeptide  
CC chains, where at least two of the chains comprise at least one heavy  
CC chain portion, and at least two of the chains comprise at least one light  
CC chain portion, a method of increasing the amount of a first polypeptide  
CC dimer relative to the amount of a second polypeptide dimer produced by a  
CC cell, a composition comprising a first polypeptide dimer, a polypeptide  
CC comprising a synthetic connecting peptide, where the polypeptide is not a  
CC naturally occurring IgG3 molecule, and a method of increasing the amount  
CC of dimers comprising polypeptide chains linked via at least one disulfide  
CC linkage in a population of IgG4 molecules produced by a cell. The  
CC composition is useful for treating a subject that would benefit from  
CC treatment with a binding molecule, where the subject is suffering from  
CC cancer, lymphoma, an autoimmune disease or disorder or an inflammatory  
CC disease or disorder. The autoimmune diseases include Crohns disease,  
CC inflammatory bowel disease, systemic lupus erythematosus, ulcerative  
CC colitis, rheumatoid arthritis, Goodpasture's syndrome, Grave's disease,  
CC Hashimoto's disease, pemphigus vulgaris, myasthenia gravis, scleroderma,  
CC autoimmune hemolytic anemia, pernicious anemia and Sjogrens syndrome.  
CC This sequence represents a heavy chain CH2 domain-deleted huCC49  
CC polypeptide, used in the scope of the invention.  
XX  
XX SQ Sequence 347 AA;  
Query Match 94.3%; Score 1770; DB 9; Length 347;  
Best Local Similarity 96.5%; Pred. No. 1e-107;  
Matches 335; Conservative 0; Mismatches 0; Indels 12; Gaps 1;  
QY 20 QVQLVQSGAEVVKPGASVKISCKASGYTFTDTHAIHWVKQNPQORLEWIGYFSGNDPFY 79  
DB 1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDTHAIHWVKQNPQORLEWIGYFSGNDPFY 60  
QY 80 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRLNMAWQOGLTVTVSSASTKG 139  
DB 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRLNMAWQOGLTVTVSSASTKG 120

QY 140 PSVFLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL 199  
DB 121 PSVFLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL 180  
QY 200 SSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKHTHCPRCP----- 247  
DB 181 SSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKHTHCPRCP----- 240  
QY 248 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 307  
DB 241 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 300  
QY 308 DGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK 354  
DB 301 DGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK 347  
RESULT 4  
ADW77049  
ID ADW77049 standard; protein; 360 AA.  
XX  
XX AC ADW77049;  
XX  
XX DT 24-MAR-2005 (first entry)  
XX  
XX DE Heavy chain CH2 domain-deleted huCC49 polypeptide #2.  
XX  
XX KW Protein production; protein purification; cancer; lymphoma;  
KW autoimmune disease; inflammation; Crohns disease;  
KW inflammatory bowel disease; systemic lupus erythematosus;  
KW ulcerative colitis; rheumatoid arthritis; Goodpasture's syndrome;  
KW Grave's disease; Hashimoto's disease; pemphigus vulgaris;  
KW myasthenia gravis; scleroderma; autoimmune hemolytic anemia;  
KW pernicious anemia; Sjogrens syndrome; immunosuppressive; antianemic;  
KW dermatological; muscular-gen.; neuroprotective; thyromimetic;  
KW antihypertoid; nephrotropic; antirheumatic; antiarthritic;  
KW antiinflammatory; antitumor; gastrointestinal-gen.; neoplasm;  
KW immune disorder; huCC49; heavy chain; antibody.  
XX  
XX OS Homo sapiens.  
OS Synthetic.  
XX WO2005000898-A2.  
XX  
XX PD 06-JAN-2005.  
XX  
XX PF 28-JUN-2004; 2004WO-US020944.  
XX  
XX PR 27-JUN-2003; 2003US-0483877P.  
PR 03-OCT-2003; 2003US-0508810P.  
PR 28-OCT-2003; 2003US-0515351P.  
PR 30-OCT-2003; 2003US-0516030P.  
XX  
XX (BIOG-) BIOGEN IDEC MA INC.  
XX  
XX PI Braslawsky GR, Glaser S, Yang T, Hopp J, Chinn P;  
XX  
XX DR WPI; 2005-058132/06.  
DR N-PSDB; ADW77047.  
XX  
XX PT New composition comprising polypeptide dimers having at least two binding  
PT sites and at least two polypeptide chains comprising a heavy chain  
PT portion and a synthetic peptide, useful for treating e.g., cancer or  
PT autoimmune diseases.  
XX  
XX PS Claim 30; SEQ ID NO 22; 152pp; English.  
XX  
XX CC The invention relates to a composition comprising polypeptide dimers  
CC having at least two binding sites and at least two polypeptide chains,  
CC where the polypeptide chains comprise at least one heavy chain portion  
CC and a synthetic connecting peptide. The invention also relates to a  
CC nucleic acid molecule comprising a nucleotide sequence encoding a

CC polypeptide chain, a host cell comprising the nucleic acid molecule, a  
CC connecting peptide, a domain deleted antibody molecule, an antibody  
CC molecule, a method of separating a first properly folded antibody  
CC molecule from a second improperly folded antibody molecule, where each of  
CC the first and second antibody molecules comprises four polypeptide  
CC chains, where at least two of the chains comprise at least one heavy  
CC chain portion, and at least two of the chains comprise at least one light  
CC chain portion, a method of increasing the amount of a first polypeptide  
CC dimer relative to the amount of a second polypeptide dimer produced by a  
CC cell, a composition comprising a first polypeptide dimer, a polypeptide  
CC comprising a synthetic connecting peptide, where the polypeptide is not a  
CC naturally occurring IgG3 molecule, and a method of increasing the amount  
CC of dimers comprising polypeptide chains linked via at least one disulfide  
CC linkage in a population of IgG4 molecules produced by a cell. The  
CC composition is useful for treating a subject that would benefit from  
CC treatment with a binding molecule, where the subject is suffering from  
CC cancer, lymphoma, an autoimmune disease or disorder or an inflammatory  
CC disease or disorder. The autoimmune diseases include Crohns disease,  
CC inflammatory bowel disease, systemic lupus erythematosus, ulcerative  
CC colitis, rheumatoid arthritis, Goodpasture's syndrome, Grave's disease,  
CC Hashimotos disease, pemphigus vulgaris, myasthenia gravis, scleroderma,  
CC autoimmune hemolytic anemia, pernicious anemia and Sjogrens syndrome.  
CC This sequence represents a heavy chain CH2 domain-deleted huCC49  
CC polypeptide, used in the scope of the invention.  
XX  
SQ Sequence 360 AA;

Query Match 94.0%; Score 1763.5; DB 9; Length 360;  
Best Local Similarity 93.1%; Pred. No. 2.8e-107;  
Matches 335; Conservative 0; Mismatches 0; Indels 25; Gaps 1;  
QY 20 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQRLEWIGYFSPGNDPKY 79  
DB 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQRLEWIGYFSPGNDPKY 60  
QY 80 NERFGKATLTADTASTAYVELSLRSEDYAVFCTRLNWAYWGQGLTVTVSSASTKG 139  
DB 61 NERFGKATLTADTASTAYVELSLRSEDYAVFCTRLNWAYWGQGLTVTVSSASTKG 120  
QY 140 PSVFFLPAPSSKSTSGTGAALGLVDYFPPEPTVTVSNWNGALTSVGHVTFPAVLQSSGLYSL 199  
DB 121 PSVFFLPAPSSKSTSGTGAALGLVDYFPPEPTVTVSNWNGALTSVGHVTFPAVLQSSGLYSL 180  
QY 200 SSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTCCPCP----- 247  
DB 181 SSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTCCPCP----- 240  
QY 248 -----GPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQP 294  
DB 241 RCPGGSGSGGGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQP 300  
QY 295 ENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKLSLSPOK 354  
DB 301 ENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKLSLSPOK 360

RESULT 5  
ADW77050  
ID ADW77050 standard; protein; 362 AA.  
XX ADW77050;  
XX  
XX 24-MAR-2005 (first entry)  
XX  
DE Heavy chain CH2 domain-deleted huCC49 polypeptide #3.  
XX  
KW Protein production; protein purification; cancer; lymphoma;  
KW autoimmune disease; inflammation; Crohns disease;  
KW inflammatory bowel disease; systemic lupus erythematosus;  
KW ulcerative colitis; rheumatoid arthritis; Goodpasture's syndrome;  
KW Grave's disease; Hashimotos disease; pemphigus vulgaris;  
KW myasthenia gravis; scleroderma; autoimmune hemolytic anemia;  
KW pernicious anemia; Sjogrens syndrome; immunosuppressive; antianemic;

KW dermatological; muscular-gen.; neuroprotective; thyromimetic;  
KW antithyroid; nephrotropic; antirheumatic; antiarthritic;  
KW antiinflammatory; antiulcer; gastrointestinal-gen.; neoplasm;  
KW immune disorder; huCC49; heavy chain; antibody.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX WO2005000898-A2.  
XX  
PD 06-JAN-2005.  
XX  
PF 28-JUN-2004; 2004WO-US020944.  
XX  
PR 27-JUN-2003; 2003US-0483877P.  
PR 03-OCT-2003; 2003US-0508810P.  
PR 28-OCT-2003; 2003US-0515351P.  
PR 30-OCT-2003; 2003US-0516030P.  
XX  
XX (BIOTG-) BIOGEN IDEC MA INC.  
PA  
PI Braslawsky GR, Glaeser S, Yang T, Hopp J, Chinn P;  
XX WPI; 2005-058132/06.  
DR N-PSDB; ADW77048.  
XX  
XX New composition comprising polypeptide dimers having at least two binding  
PT sites and at least two polypeptide chains comprising a heavy chain  
PT portion and a synthetic peptide, useful for treating e.g., cancer or  
PT autoimmune diseases.  
XX  
PS Claim 30; SEQ ID NO 23; 152pp; English.  
XX  
CC The invention relates to a composition comprising polypeptide dimers  
CC having at least two binding sites and at least two polypeptide chains,  
CC where the polypeptide chains comprise at least one heavy chain portion  
CC and a synthetic connecting peptide. The invention also relates to a  
CC nucleic acid molecule comprising a nucleotide sequence encoding a  
CC polypeptide chain, a host cell comprising the nucleic acid molecule, a  
CC connecting peptide, a domain deleted antibody molecule, an antibody  
CC molecule, a method of separating a first properly folded antibody  
CC molecule from a second improperly folded antibody molecule, where each of  
CC the first and second antibody molecules comprises four polypeptide  
CC chains, where at least two of the chains comprise at least one heavy  
CC chain portion, and at least two of the chains comprise at least one light  
CC chain portion, a method of increasing the amount of a first polypeptide  
CC dimer relative to the amount of a second polypeptide dimer produced by a  
CC cell, a composition comprising a first polypeptide dimer, a polypeptide  
CC comprising a synthetic connecting peptide, where the polypeptide is not a  
CC naturally occurring IgG3 molecule, and a method of increasing the amount  
CC of dimers comprising polypeptide chains linked via at least one disulfide  
CC linkage in a population of IgG4 molecules produced by a cell. The  
CC composition is useful for treating a subject that would benefit from  
CC treatment with a binding molecule, where the subject is suffering from  
CC cancer, lymphoma, an autoimmune disease or disorder or an inflammatory  
CC disease or disorder. The autoimmune diseases include Crohns disease,  
CC inflammatory bowel disease, systemic lupus erythematosus, ulcerative  
CC colitis, rheumatoid arthritis, Goodpasture's syndrome, Grave's disease,  
CC Hashimotos disease, pemphigus vulgaris, myasthenia gravis, scleroderma,  
CC autoimmune hemolytic anemia, pernicious anemia and Sjogrens syndrome.  
CC This sequence represents a heavy chain CH2 domain-deleted huCC49  
CC polypeptide, used in the scope of the invention.  
XX  
SQ Sequence 362 AA;

Query Match 93.9%; Score 1762.5; DB 9; Length 362;  
Best Local Similarity 92.5%; Pred. No. 3.3e-107;  
Matches 335; Conservative 0; Mismatches 0; Indels 27; Gaps 1;  
QY 20 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQRLEWIGYFSPGNDPKY 79  
DB 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQRLEWIGYFSPGNDPKY 60



```
QY 80 NERFKGKATLTADTASTAYVELSSLRSEDYVYFCTSLNLMAYWGQGLTVTVSSASTKG 139
DB 61 NERFKGKATLTADTASTAYVELSSLRSEDYVYFCTSLNLMAYWGQGLTVTVSSASTKG 120
QY 140 PSVFPLAPSSKSTSGTAAALCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL 199
DB 121 PSVFPLAPSSKSTSGTAAALCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL 180
QY 200 SSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKHTHCPPCP----- 247
DB 181 SSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKHTHCPPCP----- 240
QY 248 -----GQREPVYTLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNG 292
DB 241 RCPAPGGSGGGGQPREPVYTLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNG 300
QY 293 QPENNYKTTTPVLDSDGSEFLYSLKLVDSRWQOGNVFSCVMHEALHNHYTQKSLSLSP 352
DB 301 QPENNYKTTTPVLDSDGSEFLYSLKLVDSRWQOGNVFSCVMHEALHNHYTQKSLSLSP 360
QY 353 GK 354
DB 361 GK 362

RESULT 6
ADW44587
ID ADW44587 standard; protein; 603 AA.
XX
AC ADW44587;
XX
DT 24-MAR-2005 (first entry)
XX
DE Antibody huCC49 heavy chain (CH2 domain deleted).
XX
KW Antibody engineering; bispecific antibody; Cytostatic; Immunosuppressive;
KW Antiinflammatory; Gastrointestinal-Gen.; Dermatological; Antitumor;
KW Antirheumatic; Antiarthritic; Nephroretropic; Antithyroid; Thyromimetic;
KW Muscular-Gen.; Neuroprotective; Antianemic; CNS-Gen.; Respiratory-Gen.;
KW Vulnerary; cancer; neoplasm; lymphoma; autoimmune disease; inflammation;
KW huCC49; Tag72; heavy chain variable region.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
PN WO2005000899-A2.
XX
PD 06-JAN-2005.
XX
PF 28-JUN-2004; 2004WQ-US020945.
XX
PR 27-JUN-2003; 2003US-0483877P.
PR 03-OCT-2003; 2003US-0508810P.
PR 28-OCT-2003; 2003US-0515351P.
PR 30-OCT-2003; 2003US-0516030P.
XX
PA (BIOG-) BIOGEN IDEC MA INC.
XX
XX Glaser S, Reff M, Yang T, Wu X, Chinn P;
PI WPI; 2005-058133/06.
DR N-PSDB; ADW44584.
XX
XX New composition comprising polypeptide dimers comprising at least four
PT binding sites and at least two polypeptide chains linked via at least one
PT interchain disulfide linkage, useful for treating e.g., cancer or
PT autoimmune diseases.
XX
XX Example 8; SEQ ID NO 19; 172pp; English.
PS
XX The invention relates to a composition comprising polypeptide dimers
CC
```

```
CC comprising at least four binding sites and at least two polypeptide
CC chains, where the polypeptide chains comprise at least one heavy chain
CC portion and a synthetic connecting peptide, and where greater than about
CC 50% of the dimers comprise polypeptide chains that are linked via at
CC least one interchain disulfide linkage, or comprising minibody molecules
CC comprising two polypeptide chains, where the polypeptide chains comprise
CC a heavy chain portion and a synthetic connecting peptide, where the
CC polypeptide chains lack all or part of a CH2 domain, and where greater
CC than about 50% of the molecules are present in a form in which one of the
CC polypeptide chains are linked via at least one interchain disulfide
CC linkage. Also included are a nucleic acid molecule comprising a
CC nucleotide sequence encoding a polypeptide chain as defined above, a host
CC cell comprising a vector and a binding molecule comprising CH2 deleted
CC heavy and light chains of the antibodies huCC49 and PRIMATIZED p388. The
CC synthetic connecting peptide comprises a (Gly-Ser)n linker attached to a
CC portion of a hinge region from IGG1, IGG3 or IGG4. The molecules are
CC bispecific and comprise at least one binding site specific for a soluble
CC ligand or for a cell surface molecule. The molecules comprise two binding
CC sites specific for a tumor cell antigen and two binding sites specific
CC for a prodrug. The synthetic connecting peptide comprises a proline
CC residue at position 243, Kabat numbering system. The synthetic connecting
CC peptide further comprises an alanine residue at position 244 and a
CC proline residue at position 245, Kabat numbering system. The polypeptide
CC dimers are tetraivalent minibody molecules. The composition is useful for
CC treating a subject that would benefit from treatment with an antigen
CC binding molecule, where the subject is suffering from cancer, lymphoma,
CC an autoimmune disease or disorder, or an inflammatory disease or disorder
CC The composition is useful for treating autoimmune diseases such as
CC Crohn's disease, inflammatory bowel disease, systemic lupus
CC erythematosus, ulcerative colitis, rheumatoid arthritis, Goodpasture's
CC syndrome, Grave's disease, Hashimoto's thyroiditis, pemphigus vulgaris,
CC myasthenia gravis, scleroderma, autoimmune hemolytic anemia, pernicious
CC anemia, Sjogren's syndrome, neurological disorders such as multiple
CC sclerosis, and inflammatory diseases or disorders such as cystic
CC fibrosis, sinusitis, gastroenteritis, drug reactions and burns. The
CC polypeptide is useful for diagnostic or therapeutic purposes. The binding
CC molecules are also useful for pretargeting applications for
CC chemotherapeutic drug delivery. The present sequence represents a heavy
CC chain variable region (optionally CH2 domain deleted) from the anti-Tag72
CC antibody huCC49.
XX
XX Sequence 603 AA;
XX
Query Match 93.9%; Score 1762.5; DB 9; Length 603;
Best Local Similarity 97.1%; Pred. No. 5.8e-107;
Matches 334; Conservative 0; Mismatches 1; Indels 9; Gaps 1;
QY 20 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWMVKQNPORLEWIGYFSGNDDFKY 79
DB 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWMVKQNPORLEWIGYFSGNDDFKY 60
QY 80 NERFKGKATLTADTASTAYVELSSLRSEDYVYFCTSLNLMAYWGQGLTVTVSSASTKG 139
DB 61 NERFKGKATLTADTASTAYVELSSLRSEDYVYFCTSLNLMAYWGQGLTVTVSSASTKG 120
QY 140 PSVFPLAPSSKSTSGTAAALCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL 199
DB 121 PSVFPLAPSSKSTSGTAAALCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL 180
QY 200 SSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKHTHCPPCP-----PGQP 250
DB 181 SSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKHTHCPPCGSGSGGGGQGP 240
QY 251 REPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGPENNYKTTTPVLDSDGS 310
DB 241 REPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGPENNYKTTTPVLDSDGS 300
QY 311 FFYLSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 354
DB 301 FFYLSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 344
XX
XX RESULT 7
```

ADW44588  
ID ADW44588 standard; protein; 621 AA.  
XX  
AC ADW44588;  
DT 24-MAR-2005 (first entry)  
XX  
DE Antibody huCC49 heavy chain (CH2 domain deleted/synthetic hinge).  
XX  
XX Antibody engineering; bispecific antibody; Cytostatic; Immunosuppressive;  
KW Antinflammatory; Gastrointestinal-Gen.; Dermatological; Anticancer;  
KW Antiinflammatory; Antiarthritic; Nephrotropic; Antithyroid; Thyromimetic;  
KW Antirheumatic; Neuroprotective; Antianemic; CNS-Gen.; Respiratory-Gen.;  
KW Muscular-Gen.; Neuroprotective; Antianemic; CNS-Gen.; Respiratory-Gen.;  
KW Vulnerary; cancer; neoplasm; lymphoma; autoimmune disease; inflammation;  
KW huCC49; Tag72; heavy chain variable region.  
XX  
OS Mus sp.  
OS Homo sapiens.  
OS Synthetic.  
OS Chimeric.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 243..246  
FT /note= "Encoded by CCAGGA"  
XX  
XX WO200500899-A2.  
XX  
XX 06-JAN-2005.  
XX  
XX 28-JUN-2004; 2004WO-US020945.  
XX  
XX 27-JUN-2003; 2003US-0483877P.  
PR 03-OCT-2003; 2003US-0508810P.  
PR 28-OCT-2003; 2003US-051531P.  
PR 30-OCT-2003; 2003US-0516030P.  
XX  
XX (BIOG-) BIOGEN IDEC MA INC.  
XX  
XX Glaser S, Reff M, Yang T, Wu X, Chinn P;  
PI WPI; 2005-058133/06.  
DR N-PSDB; ADW44585.  
XX  
XX New composition comprising polypeptide dimers comprising at least four  
PT binding sites and at least two polypeptide chains linked via at least one  
PT interchain disulfide linkage, useful for treating e.g., cancer or  
PT autoimmune diseases.  
XX  
XX Claim 34; SEQ ID NO 20; 172pp; English.  
XX  
XX The invention relates to a composition comprising polypeptide dimers  
CC comprising at least four binding sites and at least two polypeptide  
CC chains, where the polypeptide chains comprise at least one heavy chain  
CC portion and a synthetic connecting peptide, and where greater than about  
CC 50% of the dimers comprise polypeptide chains that are linked via at  
CC least one interchain disulfide linkage, or comprising minibody molecules  
CC comprising two polypeptide chains, where the polypeptide chains comprise  
CC a heavy chain portion and a synthetic connecting peptide, where the  
CC polypeptide chains lack all or part of a CH2 domain, and where greater  
CC than about 50% of the molecules are present in a form in which one of the  
CC polypeptide chains are linked via at least one interchain disulfide  
CC linkage. Also included are a nucleic acid molecule comprising a  
CC nucleotide sequence encoding a polypeptide chain as defined above, a host  
CC cell comprising a vector and a binding molecule comprising CH2 deleted  
CC heavy and light chains of the antibodies huCC49 and PRIMATIZED p3E8. The  
CC synthetic connecting peptide comprises a (Gly-Ser)<sup>n</sup> linker attached to a  
CC portion of a hinge region from IgG1, IgG3 or IgG4. The molecules are  
CC bispecific and comprise at least one binding site specific for a soluble  
CC ligand or for a cell surface molecule. The molecules comprise two binding  
CC sites specific for a tumor cell antigen and two binding sites specific  
CC for a prodrug. The synthetic connecting peptide comprises a proline  
CC residue at position 243, Kabat numbering system. The synthetic connecting  
CC peptide further comprises an alanine residue at position 244 and a

CC proline residue at position 245, Kabat numbering system. The polypeptide  
CC dimers are tetraivalent minibody molecules. The composition is useful for  
CC treating a subject that would benefit from treatment with an antigen  
CC binding molecule, where the subject is suffering from cancer, lymphoma,  
CC an autoimmune disease or disorder, or an inflammatory disease or disorder  
CC The composition is useful for treating autoimmune diseases such as  
CC Crohn's disease, inflammatory bowel disease, systemic lupus  
CC erythematosus, ulcerative colitis, rheumatoid arthritis, Goodpasture's  
CC syndrome, Grave's disease, Hashimoto's thyroiditis, pemphigus vulgaris,  
CC myasthenia gravis, scleroderma, autoimmune hemolytic anemia, pernicious  
CC anemia, Sjogren's syndrome, neurological disorders such as multiple  
CC sclerosis, and inflammatory diseases or disorders such as cystic  
CC fibrosis, sinusitis, gastroenteritis, drug reactions and burns. The  
CC polypeptide is useful for diagnostic or therapeutic purposes. The binding  
CC molecules are also useful for pretargeting applications for  
CC chemotherapeutic drug delivery. The present sequence represents a heavy  
CC chain variable region (optionally CH2 domain deleted) from the anti-Tag72  
CC antibody huCC49.  
XX  
XX Sequence 621 AA;  
SQ  
Query Match 93.9%; Score 1762.5; DB 9; Length 621;  
Best Local Similarity 92.5%; Pred. No. 6e-107;  
Matches 335; Conservative 0; Mismatches 0; Indels 27; Gaps 1;  
QY 20 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAIHVKQNPQRLEWIGYRSPGNDPKY 79  
DB 1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAIHVKQNPQRLEWIGYRSPGNDPKY 60  
QY 80 NERFKGKATLTADTSASTAYVELSLRSEDITAVYFCTSLNNAYWGQGTTLTVSSASTKG 139  
DB 61 NERFKGKATLTADTSASTAYVELSLRSEDITAVYFCTSLNNAYWGQGTTLTVSSASTKG 120  
QY 140 PSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL 199  
DB 121 PSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL 180  
QY 200 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPPCP----- 247  
DB 181 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPPCP----- 240  
QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 292  
DB 241 RCPAPGGSSGGSGGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 300  
QY 293 QPENNYKTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSP 352  
DB 301 QPENNYKTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSP 360  
QY 353 GK 354  
DB 361 GK 362  
RESULT 8  
ID ADW77053 standard; protein; 362 AA.  
XX  
AC ADW77053;  
DT 24-MAR-2005 (first entry)  
XX  
DE Heavy chain CH2 domain-deleted huCC49 polypeptide #4.  
XX  
XX Protein production; protein purification; cancer; lymphoma;  
KW autoimmune disease; inflammation; Crohns disease;  
KW inflammatory bowel disease; systemic lupus erythematosus;  
KW ulcerative colitis; rheumatoid arthritis; Goodpasture's syndrome;  
KW Grave's disease; Hashimoto's disease; pemphigus vulgaris;  
KW myasthenia gravis; scleroderma; autoimmune hemolytic anemia;  
KW pernicious anemia; Sjogren's syndrome; immunosuppressive; antianemic;  
KW dermatological; muscular-gen.; neuroprotective; thyromimetic;  
KW antithyroid; nephrotropic; antirheumatic; antiarthritic;



CC prolonging the survival time of tumour-bearing animals and for treating  
CC tumours. The present sequence is human CH2 domain deleted C2B8 protein.  
CC This sequence is used in the exemplification of the invention  
XX  
SQ Sequence 360 AA;

Query Match 89.7%; Score 1683; DB 5; Length 360;  
Best Local Similarity 88.6%; Pred. No. 5.2e-102;  
Matches 319; Conservative 13; Mismatches 22; Indels 6; Gaps 1;

QY 1 MGWSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHVKQNP 60  
DB 1 MGWSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFTSYNMHWKQTP 60

QY 61 GORLEWIGYFPGNDGFKYNERFKGKATLTADTSASTAYVELSSLRSEDYAVYFCTRSLN 120  
DB 61 GRGLEWIGAIYFPGNDGTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYVCARSTY 120

QY 121 MA-----YWGCGTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 174  
DB 121 YGGDWYFNVWGAGTTVTVAASATKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180

QY 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEP 234  
DB 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEP 240

QY 235 KSCDKHTHTCPPCPGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 294  
DB 241 KSCDKHTHTCPPCPGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 300

QY 295 ENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 354  
DB 301 ENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 360

RESULT 10  
ABB2833  
ID ABB2833 standard; protein; 360 AA.  
XX  
AC ABB2833;  
XX  
XX 31-MAR-2003 (first entry)  
DT  
DT  
DE Antibody C2B8 CH2 domain deleted heavy chain.  
XX  
XX C2B8; antibody; cytostatic; antiallergic; antianemic; antiaesthetic;  
KW vstropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;  
KW thymometric; hepatotropic; haemostatic; antileprotic; antibacterial;  
KW neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer;  
KW dermatological; immunosuppressive; antiinflammatory.  
XX  
OS Homo sapiens.  
XX  
XX WO200296948-A2.  
XX  
XX 05-DEC-2002.  
XX  
XX 29-JAN-2002; 2002WO-US002374.  
XX  
XX 29-JAN-2001; 2001US-0264318P.  
PR 16-NOV-2001; 2001US-0331481P.  
PR 21-DEC-2001; 2001US-0341858P.  
XX  
XX (IDEC-) IDEC PHARM CORP.  
XX  
XX Braslawsky GR, Hanna N, Chinn P, Hariharan K;  
XX  
XX WPI; 2003-140446/13.  
DR N-PSDB; AB224017.  
XX  
XX Novel dimeric antibody useful for treating immune disorder and neoplastic  
PT disorder, has several non-covalently associated monomeric subunits.  
PT  
XX

Example 1; Fig 1B; 78pp; English.

PS The invention relates to a dimeric antibody (I) comprising several  
XX monomeric subunits, where the monomeric subunits are non-covalently  
CC associated. (I) is useful for treating a disorder, especially immune  
CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,  
CC resistant Hodgkin's disease high grade, low grade and intermediate grade  
CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),  
CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular  
CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,  
CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic  
CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,  
CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,  
CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small  
CC cleaved and large cell lymphomas, in a mammal (see AB224017 for a  
CC detailed description of the various uses of (I)). The present sequence  
XX represents the antibody C2B8 CH2 domain deleted heavy chain

SQ Sequence 360 AA;

Query Match 89.7%; Score 1683; DB 6; Length 360;  
Best Local Similarity 88.6%; Pred. No. 5.2e-102;  
Matches 319; Conservative 13; Mismatches 22; Indels 6; Gaps 1;

QY 1 MGWSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHVKQNP 60  
DB 1 MGWSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFTSYNMHWKQTP 60

QY 61 GORLEWIGYFPGNDGFKYNERFKGKATLTADTSASTAYVELSSLRSEDYAVYFCTRSLN 120  
DB 61 GRGLEWIGAIYFPGNDGTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYVCARSTY 120

QY 121 MA-----YWGCGTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 174  
DB 121 YGGDWYFNVWGAGTTVTVAASATKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180

QY 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEP 234  
DB 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEP 240

QY 235 KSCDKHTHTCPPCPGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 294  
DB 241 KSCDKHTHTCPPCPGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 300

QY 295 ENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 354  
DB 301 ENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 360

RESULT 11  
AAE27923  
ID AAE27923 standard; protein; 470 AA.

XX  
AC AAE27923;  
XX  
XX 27-DEC-2002 (first entry)  
DT  
DT  
DE Human C2B8 antibody heavy chain protein.

XX Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;  
KW neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;  
KW non-Hodgkin's lymphoma; haematologic malignancy; tumour.  
XX  
OS Homo sapiens.  
XX  
XX WO200260955-A2.  
XX  
XX 08-AUG-2002.  
XX  
XX 29-JAN-2002; 2002WO-US002373.  
XX  
XX 29-JAN-2001; 2001US-0264318P.  
PR 16-NOV-2001; 2001US-0331481P.

```
XX (IDEC-) IDEC PHARM CORP.
XX Braslawsky GR, Hanna N, Chinn P;
XX WPI; 2002-698547/75.
XX N-PSDB; AAD45752.
XX Novel domain deleted CC49 antibody reactive with tumor associated antigen
XX PT -72, or C2B8 antibody reactive with CD20, useful for treating
XX myelosuppressed patient suffering from a neoplastic disorder.
XX
XX Example 1; Fig 1A; 74pp; English.
XX
XX The present invention relates to domain deleted CC49 or C2B8 antibodies.
XX Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain
XX deleted sequence in which CH2 domain has been deleted and are reactive
XX with tumor associated antigen (TAG)-72. The C2B8 antibodies are reactive
XX with CD20 and comprise a heavy chain having a sequence of a derived
XX domain deleted C2B8 construct where the CH2 domain has been deleted.
XX Sequences of the invention are useful for imaging a neoplasm. They are
XX also useful for treating myelosuppressed patients suffering from
XX neoplastic disorder such as haematologic neoplasm, preferably non-
XX Hodgkin's lymphoma. Antibodies of the invention are also used to treat
XX neoplastic disorder, colon cancer and haematologic malignancy. They are
XX useful for reducing tumour size, inhibiting tumour growth and/or
XX prolonging the survival time of tumour-bearing animals and for treating
XX tumours. The present sequence is human C2B8 heavy chain protein. This
XX sequence is used in the exemplification of the invention
XX
XX Query Match 86.0%; Score 1614; DB 5; Length 470;
XX Best Local Similarity 67.7%; Pred. No. 2.3e-97;
XX Matches 318; Conservative 13; Mismatches 23; Indels 116; Gaps 2;
XX
XX QY 1 MGMSLILLFVAVATRVLSQVLQSGAEVVGKASGVKISCKASGVTTDTHAHHVWKNQ 60
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 1 MGMSLILLFVAVATRVLSQVLQSGAEVVGKASGVKISCKASGVTTFTSYNNHHVWKT 60
XX
XX QY 61 GQPLEWIGVPSGNDPKYNERKPKATLTADTSASTAYVELSLSEDTAVYFCTSLN 120
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 61 GRGLEWIGALYPGNGDTSYNGKPKATLTADKSSSTAYVQLSSLTSEDSAVYICARSTY 120
XX
XX QY 121 MA-----YVGQGLTVTVSSASTKGPSVFPFLAPSSKSTSGTAAAGCLVKDYPPEPTVS 174
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 121 YGQDWTFNVWGAGTTTVSSASTKGPSVFPFLAPSSKSTSGTAAAGCLVKDYPPEPTVS 180
XX
XX QY 175 WNSGALTSGVHTTFAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKKVEP 234
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 181 WNSGALTSGVHTTFAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKKAEP 240
XX
XX QY 235 KSCDKHTCTCPCP----- 247
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 241 KSCDKHTCTCPCPAPPELLGGPSVFLPDKPKDTLMISTRPEVTCVVVDVSHEDPEVKFNW 300
XX
XX QY 248 ----- 247
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 301 YVDGVEVHNKATPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIETKIS 360
XX
XX QY 248 ---GQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 304
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 361 KAKGQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
XX
XX QY 305 LDSGGSFFLYSKLTVDKSRWQQGNVPCSVNHEALHNNHYTKSLSPGK 354
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 421 LDSGGSFFLYSKLTVDKSRWQQGNVPCSVNHEALHNNHYTKSLSPGK 470
XX
XX RESULT 12
XX ABB82832
XX ID ABB82832 standard; protein; 470 AA.
XX
```

```
AC ABB82832;
XX 31-MAR-2003 (first entry)
XX Antibody C2B8 heavy chain.
XX
XX C2B8; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;
XX vsotropic; immunomodulator; prozoacide; antidiabetic; nephrotropic;
XX thymine; hepatotropic; haemostatic; antileptotic; antibacterial;
XX neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antitumor;
XX dermatological; immunosuppressive; antiinflammatory.
XX
XX Homo sapiens.
XX
XX WO200296948-A2.
XX 05-DEC-2002.
XX
XX 29-JAN-2002; 2002WO-US002374.
XX
XX 29-JAN-2001; 2001US-0264318P.
XX 16-NOV-2001; 2001US-0331481P.
XX 21-DEC-2001; 2001US-0341858P.
XX
XX (IDEC-) IDEC PHARM CORP.
XX
XX Braslawsky GR, Hanna N, Chinn P, Hariharan K;
XX WPI; 2003-140446/13.
XX N-PSDB; AB224016.
XX
XX Novel dimeric antibody useful for treating immune disorder and neoplastic
XX disorder, has several non-covalently associated monomeric subunits.
XX
XX Example 1; Fig 1A; 78pp; English.
XX
XX The invention relates to a dimeric antibody (I) comprising several
XX monomeric subunits, where the monomeric subunits are non-covalently
XX associated. (I) is useful for treating a disorder, especially immune
XX disorder, and neoplastic disorder such as relapsed Hodgkin's disease,
XX resistant Hodgkin's disease high grade, low grade and intermediate grade
XX non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),
XX lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular
XX lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,
XX AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic
XX lymphadenopathy, small lymphocytic, follicular, diffuse large cell,
XX diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,
XX small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small
XX cleaved and large cell lymphomas, in a mammal. (I) is also useful for
XX treating allergic rhinitis, autoimmune haemolytic anemia, allergic
XX contact dermatitis, Addison's disease, atopic dermatitis, amyloidosis,
XX aplastic anemia, arthritis, asthma, ataxia-telangiectasia, autoimmune
XX oophoritis, Buerger's disease, bronchitis, candidiasis, Post-myocardial
XX infarction syndrome, carditis, celiac sprue, Chagas's disease, Chediak-
XX Higashi syndrome, Crohn's disease, cryoglobulinemia, diabetes mellitus,
XX erythema multiforme, glomerulonephritis, Goodpasture's syndrome, Grave's
XX disease, Hashimoto's thyroiditis, haemolytic disease of the newborn,
XX hepatitis, idiopathic thrombocytopenic purpura, leprosy, Lyme disease,
XX multiple sclerosis, myasthenia gravis, polymyositis, scleroderma,
XX paroxysmal nocturnal haemoglobinuria, psoriasis, Raynaud's phenomenon/
XX syndrome, rheumatoid arthritis, Sjogren's syndrome, systemic lupus
XX erythematosus, transplant rejection, and ulcerative colitis. (I) is also
XX useful for inducing hyper-cross-linking of membrane antigens, for killing
XX or inhibiting selected cell populations in the treatment of diseases such
XX as cancer and immune disorders, for treating myelosuppressed or
XX myelocompromised patients, for inducing apoptosis in the target cell
XX population or effectively block cell surface receptors necessary for the
XX growth of neoplastic cells, in viral or bacterial neutralization, for
XX diagnostic imaging of tumours, and for reducing tumour size, inhibiting
XX tumour growth and/or prolonging the survival time of tumour-bearing
XX animals. The present sequence represents the antibody C2B8 heavy chain
XX
XX Sequence 470 AA;
```

Query Match 86.0%; Score 1614; DB 6; Length 470;  
Best Local Similarity 67.7%; Pred. No. 2.3e-97; Mismatches 23; Indels 116; Gaps 2;  
Matches 318; Conservative 13;

QY 1 MGWSLILFLVAVATRVLSQVLQVSGAEVVKPGASVKISCKASGYTFTDHAHVKQNP 60  
DB 1 MGWSLILFLVAVATRVLSQVLQVSGAEVVKPGASVKISCKASGYTFTSYNHWKQTP 60

QY 61 GQRLWIGYFSGNDGDFKYNRPKATLTADTSASTAYVELSSLRSEDYAVYFCTRSLN 120  
DB 61 GRGLEWIGAIYFNGGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARSTY 120

QY 121 MA-----YWGOGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVTS 174  
DB 121 YGGDWYFNYWGAGTTVTVSAATKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVTS 180

QY 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNTKVDKVEP 234  
DB 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNTKVDKVEP 240

QY 235 KSCDKHTHTCPPCP----- 247  
DB 241 KSCDKHTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300

QY 248 ----- 247  
DB 301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360

QY 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 304  
DB 361 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420

QY 305 LPSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 354  
DB 421 LPSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 470

RESULT 13  
AAMS2156  
ID AAMS2156 standard; protein; 731 AA.  
AC AAMS2156;  
XX  
DT 05-FEB-2002 (first entry)  
XX  
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 1.  
XX  
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;  
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.  
XX  
OS Homo sapiens.  
XX Synthetic.  
XX  
PN WO200174905-A1.  
XX  
PD 11-OCT-2001.  
XX  
PF 26-MAR-2001; 2001WO-GB001324.  
XX  
PR 03-APR-2000; 2000GB-00008049.  
PR 02-OCT-2000; 2000US-0237159P.  
XX  
XX (ANTI-) ANTISOMA RES LTD.  
PA  
PA  
XX Young RJ;  
XX  
XX WPI; 2001-662969/76.  
XX  
PT Novel compound used to treat cancer has target cell-specific portion  
PT comprising humanized monoclonal antibody having specificity for  
PT polymorphic epithelial mucin, and cytotoxic portion having  
PT endonucleolytic activity.

XX Claim 20; Fig 7; 176pp; English.  
PS  
XX The invention relates to a compound which comprises a target cell-  
CC specific portion, comprising a humanised monoclonal antibody, having  
CC specificity for polymorphic epithelial mucin (PEM) or its antigen binding  
CC fragment and a cytotoxic portion having endonucleolytic activity,  
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02738. The  
CC compound has cytostatic activity useful for treating cancer and acting as  
CC a potential inducer of apoptosis  
XX  
SQ Sequence 731 AA;  
Query Match 86.0%; Score 1613.5; DB 4; Length 731;  
Best Local Similarity 67.7%; Pred. No. 4e-97; Mismatches 18; Indels 113; Gaps 2;  
Matches 316; Conservative 18;

QY 1 MGWSLILFLVAVATRVLSQVLQVSGAEVVKPGASVKISCKASGYTFTDHAHVKQNP 60  
DB 1 MGWSLILFLVATATGVHSQVLQVSGAEVVKPGASVKISCKASGYTFSAYWVQAP 60

QY 61 GQRLWIGYFSGNDGDFKYNRPKATLTADTSASTAYVELSSLRSEDYAVYFCTRSLN 120  
DB 61 GRGLEWVGELILPGSNRYNPKGRVTVTRDTSTNTAYMELSSLRSEDYAVYCARSYD 120

QY 121 ---MAYWOGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS 177  
DB 121 FAWFAYWOGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS 180

QY 178 GALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSC 237  
DB 181 GALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSC 240

QY 238 DKHTHTCPPCP----- 247  
DB 241 DKHTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 300

QY 248 ----- 247  
DB 301 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 360

QY 248 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 307  
DB 361 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 420

QY 308 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 354  
DB 421 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 467

RESULT 14  
AAMS2159  
ID AAMS2159 standard; protein; 741 AA.  
XX  
AC AAMS2159;  
XX  
DT 05-FEB-2002 (first entry)  
XX  
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 4.  
XX  
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;  
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200174905-A1.  
XX  
PD 11-OCT-2001.  
XX  
PF 26-MAR-2001; 2001WO-GB001324.  
XX  
XX 03-APR-2000; 2000GB-00008049.



PR 02-OCT-2000; 2000US-0237159P.  
XX (ANTI-) ANTISOMA RES LTD.  
XX  
XX Young RJ;  
XX WPI; 2001-662969/76.  
XX Novel compound used to treat cancer has target cell-specific portion  
PT comprising humanized monoclonal antibody having specificity for  
PT polymorphic epithelial mucin, and cytotoxic portion having  
PT endonucleolytic activity.  
XX Claim 20; Fig 10; 176pp; English.  
XX The invention relates to a compound which comprises a target cell-  
CC specific portion, comprising a humanized monoclonal antibody, having  
CC specificity for polymorphic epithelial mucin (PEM) or its antigen binding  
CC fragment and a cytotoxic portion having endonucleolytic activity.  
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The  
CC compound has cytostatic activity useful for treating cancer and acting as  
CC a potential inducer of apoptosis  
XX  
XX Sequence 741 AA;  
SQ  
Query Match 86.0%; Score 1613.5; DB 4; Length 741;  
Best Local Similarity 67.7%; Pred. No. 4.1e-97;  
Matches 316; Conservative 18; Mismatches 20; Indels 113; Gaps 2;  
QY 1 MGWSLILFLVANATRVLSQVQLVQSGAEVVKPGASVKISKASGYTTTDDHAIHWKQP 60  
DB 1 MGWSLILFLVANATRVLSQVQLVQSGAEVVKPGASVKISKASGYTTTDDHAIHWKQP 60  
QY 61 GORLEWIGVSPGNDKYNRFGKATLTADTSASTAYVELLSRSDTAVYFCTSLN 120  
DB 61 GRLEWVGEILPGSNRSYNEKRGVTRDTSTNTAYVELLSRSDTAVYCARSD 120  
QY 121 ---MAYWQGGTLVTYSSASTKGPSYFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS 177  
DB 121 FAWPAYWGQTLVTYSSASTKGPSYFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS 180  
QY 178 GALTSGVTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSNKVDKVEPKSC 237  
DB 181 GALTSGVTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSNKVDKVEPKSC 240  
QY 238 DKTHCTCPCP----- 247  
DB 241 DKTHCTCPCPAPELLGGFVFLPPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYVD 300  
QY 248 ----- 247  
DB 301 GVEVHNATKPREQYNSTYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAK 360  
QY 248 GQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 307  
DB 361 GQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 420  
QY 308 DGSFPLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTOKLSLSLSPGK 354  
DB 421 DGSFPLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTOKLSLSLSPGK 467  
RESULT 15  
AAB08026  
ID AAB08026 standard; protein; 470 AA.  
XX AAB08026;  
XX  
XX 12-SEP-2003 (revised)  
DT 14-NOV-2000 (first entry)  
XX  
XX A dimeric anti-CD20 heavy chain polypeptide.

KW Anti-CD20 antibody; dimeric immunoglobulin; immunoglobulin; IgG;  
KW complement system; Fc gamma receptor; cytotoxic effector cell;  
KW host immune cell; programmed cell death; allergic disorder; cancer;  
KW autoimmune disease; allergic asthma; atopic dermatitis; Crohn's disease;  
KW allergic bronchopulmonary aspergillosis; allergic rhinitis;  
KW Graves's disease; food allergy; allergic contact dermatitis; cancer;  
KW B-cell lymphoma; rheumatoid arthritis; ulcerative colitis; psoriasis;  
KW pigeon breeder's disease; hepatitis; leprosy; Lyme disease;  
KW diabetes mellitus; candidiasis; aplastic anaemia.  
XX Homo sp.  
OS Homo sapiens.  
OS Chimeric.  
XX  
XX Key Location/Qualifiers  
FT Peptide 1..19  
FT /note= "signal peptide"  
FT Protein 20..140  
FT /note= "murine anti-human CD20 heavy chain variable  
FT region"  
FT Protein 141..470  
FT /note= "human gamma 1 heavy chain constant region"  
XX  
XX WO200044788-A1.  
XX  
XX 03-AUG-2000.  
XX  
XX 28-JAN-2000; 2000WO-US001893.  
XX  
XX 28-JAN-1999; 98US-00238741.  
XX (IDEC-) IDEC PHARM CORP.  
XX  
XX Braslawsky GR, Hanna N, Hariharan K, Labarre MJ, Huynh TB;  
XX WPI; 2000-514811/46.  
XX N-PSDB; AAA63531.  
XX Genetically engineering immunoglobulin (Ig) G/IgG dimers for the  
XX treatment of cancers, allergic disorders and autoimmune conditions.  
XX  
XX Example 1; Fig 2A-C; 65pp; English.  
XX The present sequence represents a dimeric anti-CD20 light chain  
XX polypeptide. The dimeric immunoglobulin is used in the method of an  
XX invention. The specification describes a method for producing an  
XX immunoglobulin (Ig) G/IgG dimer. The method comprises genetically  
XX engineering a monoclonal antibody to introduce a cysteine molecule which  
XX inhibits formation of intramolecular disulphide bridges between sister  
XX heavy chains on the same antibody molecule. The dimer is a homodimer or  
XX heterodimer that is capable of activating components of the complement  
XX system, and has the ability to activate and kill cells via the complement  
XX cascade. The dimer is also capable of binding to Fc gamma receptors on  
XX cytotoxic effector cells and on host immune cells, and is capable of  
XX initiating programmed cell death. The IgG/IgG dimers may be used to treat  
XX allergic disorders, cancers and autoimmune diseases such as allergic  
XX asthma, allergic bronchopulmonary aspergillosis, allergic rhinitis,  
XX atopic dermatitis, Crohn's disease, Graves's disease, food allergies,  
XX allergic contact dermatitis, CLL cancers and/or B-cell lymphomas. They  
XX may also be used to treat a range of other diseases and disorders such as  
XX rheumatoid arthritis, ulcerative colitis, psoriasis, pigeon breeder's  
XX disease, hepatitis, leprosy, Lyme disease, diabetes mellitus, candidiasis  
XX and aplastic anaemia. They are also useful for inducing hyper-cross-  
XX linking of membrane antigens and for the preferential killing of selected  
XX cell populations. (Updated on 12-SEP-2003 to standardise OS field)  
XX  
XX Sequence 470 AA;  
SQ  
Query Match 86.0%; Score 1613; DB 3; Length 470;  
Best Local Similarity 67.7%; Pred. No. 2.7e-97;  
Matches 318; Conservative 13; Mismatches 23; Indels 116; Gaps 2;  
QY 1 MGWSLILFLVANATRVLSQVQLVQSGAEVVKPGASVKISKASGYTTTDDHAIHWKQP 60



```
Db      1  MGNLSILLFLVAVATRLVSQVLOQPQGAELVKPGASVWMSCKASGYTTTSYNMHWKQTP 60
Qy      61  GORLEWIGYFSPGNDDFKYNERFKGKATLTADTSAAYVELSSLRSEDTAIFYCTRSLN 120
Db      61  GRGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARSTY 120
Qy     121  MA-----YWGQGTTLVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 174
Db     121  YGGMWYFNWVGAGTTVTVAASATKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
Qy     175  WNSGALTSGVHTFPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHRKPSNTKVDKKVEP 234
Db     181  WNSGALTSGVHTFPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHRKPSNTKVDKKVEP 240
Qy     235  KSCDKTHTCPCPP----- 247
Db     241  KSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Qy     248  ----- 247
Db     301  YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
Qy     248  ---GOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 304
Db     361  KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
Qy     305  LDSGGSFELYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 354
Db     421  LDSGGSFELYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLCPGK 470
```

Search completed: February 16, 2006, 10:17:39  
Job time : 197.879 secs

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OM protein - protein search, using sw model

Run on: February 16, 2006, 10:38:47 ; Search time 92.5253 Seconds  
(without alignments)  
1083.802 Million cell updates/sec

Title: US-10-058-069-9  
Perfect score: 1243  
Sequence: 1 MDSQAQVLMMLLLVSGTCS.....EVTHQGLSSPVTKSFNRGEC 240

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*

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6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pgp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1166	93.8	240	3	US-09-301-593-28 Sequence 28, Appl
2	1166	93.8	240	4	US-10-159-006-28 Sequence 28, Appl
3	1140	91.7	220	5	US-10-880-028-19 Sequence 19, Appl
4	1140	91.7	220	5	US-10-880-320-19 Sequence 19, Appl
5	1136	91.4	240	3	US-09-301-593-36 Sequence 36, Appl
6	1136	91.4	240	4	US-10-159-006-36 Sequence 36, Appl
7	1135	91.3	220	5	US-10-880-028-27 Sequence 27, Appl
8	1135	91.3	220	5	US-10-880-320-27 Sequence 27, Appl
9	1125.5	90.5	239	6	US-10-723-003-14 Sequence 14, Appl
10	1125.5	90.5	239	6	US-11-004-639-14 Sequence 14, Appl
11	1125	90.5	240	4	US-09-799-514-8 Sequence 8, Appl
12	1122	90.3	240	4	US-10-630-406-8 Sequence 8, Appl
13	1122	90.3	240	6	US-11-073-453-8 Sequence 8, Appl
14	1121.5	90.2	239	3	US-09-249-011A-22 Sequence 22, Appl
15	1119.5	90.1	241	6	US-11-031-485-62 Sequence 62, Appl
16	1115	89.7	240	5	US-10-938-353-24 Sequence 24, Appl
17	1105.5	88.9	241	6	US-11-031-485-24 Sequence 24, Appl
18	1082	87.0	220	5	US-10-644-277-20 Sequence 20, Appl
19	1070	86.1	220	3	US-09-301-593-17 Sequence 17, Appl
20	1070	86.1	220	4	US-10-159-006-17 Sequence 17, Appl
21	1064	85.6	220	3	US-09-995-693-1 Sequence 1, Appl
22	1064	85.6	220	4	US-10-232-408-1 Sequence 1, Appl
23	1064	85.6	220	5	US-10-644-277-92 Sequence 92, Appl
24	1064	85.6	238	6	US-11-013-537-1 Sequence 1, Appl
25	1063	85.5	220	5	US-10-644-277-40 Sequence 40, Appl
26	1059	85.2	220	5	US-10-644-277-68 Sequence 68, Appl
27	1054	84.8	220	5	US-10-644-277-4 Sequence 4, Appl

28	1047	84.2	239	3	US-09-825-012-9	Sequence 9, Appl
29	1044	84.0	242	3	US-09-819-266-26	Sequence 26, Appl
30	1040	83.7	238	4	US-10-171-452A-38	Sequence 38, Appl
31	1040	83.7	238	4	US-10-171-452A-56	Sequence 56, Appl
32	1040	83.7	238	4	US-10-353-708-38	Sequence 38, Appl
33	1040	83.7	238	4	US-10-353-708-56	Sequence 56, Appl
34	1040	83.7	238	4	US-10-731-984-3	Sequence 3, Appl
35	1040	83.7	238	4	US-10-731-984-27	Sequence 27, Appl
36	1030	82.9	238	4	US-10-171-452A-44	Sequence 44, Appl
37	1030	82.9	238	4	US-10-171-452A-50	Sequence 50, Appl
38	1030	82.9	238	4	US-10-353-708-44	Sequence 44, Appl
39	1030	82.9	238	4	US-10-353-708-50	Sequence 50, Appl
40	1030	82.9	238	4	US-10-731-984-11	Sequence 11, Appl
41	1030	82.9	238	4	US-10-731-984-19	Sequence 19, Appl
42	1016.5	81.8	241	5	US-10-723-003-22	Sequence 22, Appl
43	1016.5	81.8	241	6	US-11-004-639-22	Sequence 22, Appl
44	1014.5	81.6	238	4	US-10-467-253-14	Sequence 14, Appl
45	1010.5	81.3	235	5	US-10-938-353-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1  
US-09-301-593-28  
; Sequence 28, Application US/09301593A  
; Publication No. US20020052480A1  
; GENERAL INFORMATION:  
; APPLICANT: Park, John E.  
; APPLICANT: Garin-Chesa, Pilar  
; APPLICANT: Bamberger, Uwe  
; APPLICANT: Legier, Olivier  
; APPLICANT: Saldanha, Jose W.  
; APPLICANT: Rettig, Wolfgang J.  
; TITLE OF INVENTION: FAB-specific Antibody with Improved Producibility  
; FILE REFERENCE: 0652.1890001  
; CURRENT APPLICATION NUMBER: US/09/301,593A  
; CURRENT FILING DATE: 1999-04-29  
; EARLIER APPLICATION NUMBER: EP 98107925.4  
; EARLIER FILING DATE: 1998-04-30  
; EARLIER APPLICATION NUMBER: US 60/086,049  
; EARLIER FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-301-593-28

Query Match	93.8%	Score 1166;	DB 3;	Length 240;
Best Local Similarity	93.3%	Pred. No. 1.7e-64;		
Matches	224;	Conservative	9;	Mismatches 7;
Indels	0;	Gaps	0;	
QY	1	MDSQAQVLMMLLLVSGTCDIVMSQSPDSLAVSLGERTVLTNCKSSQSLLYSQNKYLA	60	
Db	1	MDSQAQVLMMLPLVWSGTCDIVMSQSPSSLAVSVGKVTMSCKSSQSLLYSRNKYLA	60	
QY	61	WYQOKPGQSPKLLIYWASARESGVDPDRFSGSGGTDFTLTITSSVQAEADVAVVYCCQVYSY	120	
Db	61	WYQOKPGQSPKLLIFWASREGVDPDRFSGSGGTDFTLTITSSVQAEADVAVVYCCQVFSY	120	
QY	121	PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL	180	
Db	121	PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL	180	
QY	181	QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	240	
Db	181	QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	240	
RESULT 2				
US-10-159-006-28				





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Db 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKYLAWYQKPGQPKLLIYWASAR 60
QY 81 ESGVDRFSGSGSGDFTLTSSVQAEADVAVVYCOQYYSYPLTFGAGTKLELKRVAAPS 140
Db 61 ESGVDRFSGSGSGDFTLTSSVQAEADVAVVYCOQYYSYPLTFGAGTKLELKRVAAPS 120
QY 141 VFIFPPSDEQLKSGTASVVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYTS 200
Db 121 VFIFPPSDEQLKSGTASVVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYTS 180
QY 201 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220
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RESULT 8

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US-10-880-320-27
; Sequence 27, Application US/10880320
; Publication No. US20050163783A1
; GENERAL INFORMATION:
; APPLICANT: BRASLAWSKY, Gary R.
; APPLICANT: GLASER, Scott
; APPLICANT: YANG, Izung-Hornig
; APPLICANT: HOPP, Jennifer
; APPLICANT: CHINN, Paul
; TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS
; OF BINDING POLYPEPTIDES
; FILE REFERENCE: IDV-001
; CURRENT APPLICATION NUMBER: US/10/880,320
; CURRENT FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: 60/483877
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/508810
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/515351
; PRIOR FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: 60/516030
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-880-320-27
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Query Match 91.3%; Score 1135; DB 5; Length 220;
Best Local Similarity 99.5%; Pred. No. 1.3e-62;
Matches 219; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKYLAWYQKPGQPKLLIYWASAR 80
Db 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKYLAWYQKPGQPKLLIYWASAR 60
QY 81 ESGVDRFSGSGSGDFTLTSSVQAEADVAVVYCOQYYSYPLTFGAGTKLELKRVAAPS 140
Db 61 ESGVDRFSGSGSGDFTLTSSVQAEADVAVVYCOQYYSYPLTFGAGTKLELKRVAAPS 120
QY 141 VFIFPPSDEQLKSGTASVVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYTS 200
Db 121 VFIFPPSDEQLKSGTASVVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYTS 180
QY 201 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220
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RESULT 9

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US-10-723-003-14
; Sequence 14, Application US/10723003
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; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-723-003-14
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Query Match 90.5%; Score 1125.5; DB 5; Length 239;
Best Local Similarity 89.6%; Pred. No. 5.3e-62;
Matches 215; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

QY 1 MDSQAQVLMLLLVVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKYL 60
Db 1 MESQTQVFLSLLLVVSGTCGNIWMTQSPSSLAVSAGEKVTMTSCKSSQSLVYSSNQKYL 60
QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGSGDFTLTSSVQAEADVAVVYCOQYYS 120
Db 61 WYQKPGQSPKLLIYWASTRESGVDPDRFTGSGSGDFTLTSSVQAEADVAVVYCHQYFS 119
QY 121 PLTFGAGTKLELKRVAAPSVFIPPPSDEQLKSGTASVVCLNNFYPREAKVQWVDNAL 180
Db 120 SYTFGGGTKLEIKRTVAAPSVFIPPPSDEQLKSGTASVVCLNNFYPREAKVQWVDNAL 179
QY 181 QSGNSQESVTEQDSKDYTSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 180 QSGNSQESVTEQDSKDYTSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
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RESULT 10

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US-11-004-639-14
; Sequence 14, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/11/004,639
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-004-639-14
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Query Match 90.5%; Score 1125.5; DB 6; Length 239;

Best Local Similarity 89.6%; Pred. No. 5.3e-62;  
Matches 215; Conservative 13; Mismatches 11; Indels 1; Gaps 1;  
Qy 1 MDSQAQVLMLLLVWVSGTCGDIWMSQSPDSLAVSLGSRVTLNCKSSOSLLYSGNQKNYLA 60  
Db 1 MESQTQVFLSJLLWVSGTCGNIWMTQSPSSLAVSAGEKVTMSKSSQSVLYSSNQKNYLA 60  
Qy 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDTLTITSSVQAEADVAVYCCQYYSY 120  
Db 61 WYQKPGQSPKLLIYWASTRESGVDPDRFTGSGSGTDTLTITSSVQAEADVAVYCHQYFS- 119  
Qy 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL 180  
Db 120 SYTFGGGTGLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL 179  
Qy 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 240  
Db 180 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 11  
US-09-799-514-8  
; Sequence 8, Application US/09799514  
; Patent No. US20020065220A1  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and Ar  
; FILE REFERENCE: PT015P1  
; CURRENT APPLICATION NUMBER: US/09/799,514  
; CURRENT FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: PCT/US00/23662  
; PRIOR FILING DATE: 2000-08-29  
; PRIOR APPLICATION NUMBER: 60/152,248  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-799-514-8

Query Match 90.5%; Score 1125; DB 3; Length 240;  
Best Local Similarity 90.3%; Pred. No. 5.7e-62;  
Matches 214; Conservative 10; Mismatches 13; Indels 0; Gaps 0;  
Qy 4 QAOVLMLLLVWVSGTCGDIWMSQSPDSLAVSLGSRVTLNCKSSOSLLYSGNQKNYLA 63  
Db 4 QTQVFISLLWISGAYGDIWMTQSPDSLAVSLGSRVTLNCKSSQTVLYSSDNKNYLA 63  
Qy 64 QKPGQSPKLLIYWASARESGVDPDRFSGSGGTDTLTITSSVQAEADVAVYCCQYYSYPLT 123  
Db 64 QKPGQSPKLLIYWASTRESGVDPDRFSGSGGTDTLTITSSVQAEADVAVYCCQYYSYTPS 123  
Qy 124 FGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSG 183  
Db 124 FGQGTGLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSG 183  
Qy 184 NSQESVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 240  
Db 184 NSQESVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 12  
US-10-630-406-8  
; Sequence 8, Application US/10630406  
; Publication No. US20040105855A1  
; GENERAL INFORMATION:  
; APPLICANT: Jure-Kunkel, Maria  
; APPLICANT: Ganguly, Subinay  
; APPLICANT: Abraham, Ralph  
; APPLICANT: Hollenbaugh, Diane L.  
; APPLICANT: Rillema, Jill

; APPLICANT: Thorne, Barbara  
; APPLICANT: Shuford, Walter W.  
; APPLICANT: Mittler, Robert S.  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN 4-1BB  
; FILE REFERENCE: D0288 NP  
; CURRENT APPLICATION NUMBER: US/10/630,406  
; CURRENT FILING DATE: 2003-07-30  
; PRIOR APPLICATION NUMBER: US 60/399,646  
; PRIOR FILING DATE: 2002-07-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-630-406-8

Query Match 90.3%; Score 1122; DB 4; Length 240;  
Best Local Similarity 90.0%; Pred. No. 8.8e-62;  
Matches 216; Conservative 10; Mismatches 14; Indels 0; Gaps 0;  
Qy 1 MDSQAQVLMLLLVWVSGTCGDIWMSQSPDSLAVSLGSRVTLNCKSSOSLLYSGNQKNYLA 60  
Db 1 MEAPQQLFLLLLWLPDPTGDIWMTQSPDSLAVSLGSRVTLNCKSSOSLLSSGNQKNYLA 60  
Qy 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDTLTITSSVQAEADVAVYCCQYYSY 120  
Db 61 WYQKPGQSPKLLIYASTRQSGVDPDRFSGSGGTDTLTITSSVQAEADVAVYCYLDYRY 120  
Qy 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL 180  
Db 121 PFTFGQGTGLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL 180  
Qy 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 240  
Db 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 13  
US-11-073-453-8  
; Sequence 8, Application US/11073453  
; Publication No. US2005020202A1  
; GENERAL INFORMATION:  
; APPLICANT: Jure-Kunkel, Maria  
; APPLICANT: Ganguly, Subinay  
; APPLICANT: Abraham, Ralph  
; APPLICANT: Hollenbaugh, Diane L.  
; APPLICANT: Rillema, Jill  
; APPLICANT: Thorne, Barbara  
; APPLICANT: Shuford, Walter W.  
; APPLICANT: Mittler, Robert S.  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN 4-1BB  
; FILE REFERENCE: D0288 NP  
; CURRENT APPLICATION NUMBER: US/11/073,453  
; CURRENT FILING DATE: 2005-03-07  
; PRIOR APPLICATION NUMBER: US 60/399,646  
; PRIOR FILING DATE: 2002-07-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-11-073-453-8

Query Match 90.3%; Score 1122; DB 6; Length 240;  
Best Local Similarity 90.0%; Pred. No. 8.8e-62;  
Matches 216; Conservative 10; Mismatches 14; Indels 0; Gaps 0;





GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 16, 2006, 10:39:32 ; Search time 8.88889 Seconds  
(without alignments)  
383.795 Million cell updates/sec

Title: US-10-058-069-9  
Perfect score: 1243  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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8: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1043.5	84.0	666	6	US-10-981-356A-29
2	1043.5	84.0	667	7	US-11-096-046-29
3	1040	83.7	238	7	US-11-158-505-1
4	1040	83.7	238	7	US-11-158-505-3
5	1040	83.7	238	7	US-11-158-505-25
6	1040	83.7	238	7	US-11-158-505-27
7	1030	82.9	238	7	US-11-158-505-9
8	1030	82.9	238	7	US-11-158-505-11
9	1030	82.9	238	7	US-11-158-505-17
10	1030	82.9	238	7	US-11-158-505-19
11	1030	82.9	238	7	US-11-158-505-74
12	1000.5	80.5	666	6	US-10-981-356A-25
13	1000.5	80.5	666	6	US-10-981-356A-27
14	1000.5	80.5	666	6	US-10-981-356A-28
15	1000.5	80.5	666	7	US-11-096-046-27
16	1000.5	80.5	667	7	US-11-096-046-25
17	1000.5	80.5	667	7	US-11-096-046-28
18	1000.5	80.5	692	6	US-10-981-356A-26
19	1000.5	80.5	695	7	US-11-096-046-26
20	994.5	80.0	235	7	US-11-128-900-14
21	994.5	80.0	235	7	US-11-128-900-65
22	992	79.8	218	7	US-11-158-505-4
23	992	79.8	218	7	US-11-158-505-28
24	991.5	79.8	233	7	US-11-128-900-15
25	991.5	79.8	233	7	US-11-128-900-67

26	985	79.2	234	7	US-11-128-900-17	Sequence 17, Appl
27	985	79.2	234	7	US-11-128-900-69	Sequence 69, Appl
28	982.5	79.0	666	6	US-10-981-356A-30	Sequence 30, Appl
29	982.5	79.0	667	7	US-11-096-046-30	Sequence 30, Appl
30	982	79.0	218	7	US-11-158-505-12	Sequence 12, Appl
31	982	79.0	218	7	US-11-158-505-20	Sequence 20, Appl
32	982	79.0	236	7	US-11-086-289-20	Sequence 20, Appl
33	978.5	78.7	235	7	US-11-086-289-16	Sequence 16, Appl
34	977	78.6	236	7	US-11-086-289-8	Sequence 8, Appl
35	970.5	78.1	239	7	US-11-177-648-10	Sequence 10, Appl
36	967.5	77.8	238	7	US-11-177-648-35	Sequence 35, Appl
37	966	77.7	236	7	US-11-144-248-48	Sequence 48, Appl
38	966	77.7	236	7	US-11-144-222-48	Sequence 48, Appl
39	966	77.7	236	7	US-11-182-343-48	Sequence 48, Appl
40	963.5	77.5	238	7	US-11-177-648-80	Sequence 80, Appl
41	962	77.4	236	7	US-11-144-248-52	Sequence 52, Appl
42	962	77.4	236	7	US-11-144-222-52	Sequence 52, Appl
43	962	77.4	236	7	US-11-182-343-52	Sequence 52, Appl
44	961	77.3	236	7	US-11-086-289-4	Sequence 4, Appl
45	960.5	77.3	238	7	US-11-177-648-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1  
US-10-981-356A-29  
; Sequence 29, Application US/10981356A  
; Publication No. US20060015952A1  
; GENERAL INFORMATION:  
; APPLICANT: FILVAROFF, ELLEN H.  
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT  
; FILE REFERENCE: P2068R1  
; CURRENT APPLICATION NUMBER: US/10/981.356A  
; CURRENT FILING DATE: 2004-11-04  
; PRIOR APPLICATION NUMBER: US 60/520,398  
; PRIOR FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: US 60/557,951  
; PRIOR FILING DATE: 2004-03-31  
; NUMBER OF SEQ ID NOS: 45  
; SEQ ID NO 29  
; LENGTH: 666  
; TYPE: PRI  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence is synthesized  
US-10-981-356A-29

Query Match	84.0%	Score	1043.5	DB	6	Length	666
Best Local Similarity	91.4%	Pred. No.	2.6e-61				
Matches	201	Conservative	9	Mismatches	9	Indels	1
Gaps	1						
Qy	21	DIWMSQSPDSLAVSLGERVTLNCKSSQSLAYSGNKNYLAWYQKPGSQSKLLIYASAR	80				
Db	1	DIWMTQSPSSSLAVSAGEKVTMSKSSQSVLYSSNQKNYLAWYQKPGSQSKLLIYASTR	60				
Qy	81	ESGVPRFSGSGGTFTLTITSSVQAEADVAVYCCQYYSYPLTFGAGTKLEKRTVAAPS	140				
Db	61	ESGVPRDFTGSGSGTFTLTITSSVQAEADVAVYCHQYVSSD-TFGGCTKLEIKRTVAAPS	119				
Qy	141	VFIFFPSDEQLKSGTASVCLLNFPYFPAKQVQKVDNALQSGNSQSVTEQDSKDSYTS	200				
Db	120	VFIFFPSDEQLKSGTASVCLLNFPYFPAKQVQKVDNALQSGNSQSVTEQDSKDSYTS	179				
Qy	201	LSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC	240				
Db	180	LSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC	219				

RESULT 2  
US-11-096-046-29  
; Sequence 29, Application US/11096046  
; Publication No. US20050276802A1

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; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROPF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 29
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; NAME/KEY: Unsure
; LOCATION: 220
; OTHER INFORMATION: Unknown amino acid
; US-11-096-046-29

Query Match      84.0%; Score 1043.5; DB 7; Length 667;
Best Local Similarity 91.4%; Pred. No. 2.6e-61;
Matches 201; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

QY 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 80
DB 1 DIWMTQSPSLAVSAGEKVTMSCKSSQSLYSSNQKNYLAWYQKPGQSPKLLIYWASTR 60

QY 81 ESGVPRFSGSGGTDFLTITSSVQAEADVAVYVCOQYYSPLTFGAGTKLELKRVTAA 140
DB 61 ESGVPRFSGSGGTDFLTITSSVQAEADVAVYVCOQYYSPLTFGAGTKLELKRVTAA 119

QY 141 VFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDY 200
DB 120 VFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDY 179

QY 201 LSSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 240
DB 180 LSSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 219

RESULT 3
US-11-158-505-1
; Sequence 1, Application US/11158505
; Publication No. US2006002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 1
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody light chain construct
; US-11-158-505-1

Query Match      83.7%; Score 1040; DB 7; Length 238;
Best Local Similarity 84.6%; Pred. No. 1.8e-61;
Matches 203; Conservative 15; Mismatches 20; Indels 2; Gaps 1;

QY 1 MDSQAQVLMLLLVWSGTGDI VMSQSPDSLAVSLGERVTLNCKSSQSLYSGNQKNYLA 60
DB 1 METDTILLWLLWVPGSTGDI VMTQSPDSLAVSLGERATINCASQSDYDGD--SYMN 58

QY 61 WYQKPGQSPKLLIYWASARESGVPRFSGSGGTDFLTITSSVQAEADVAVYVCOQYYS 120
DB 59 WYQKPGQSPKLLIYWASARESGVPRFSGSGGTDFLTITSSVQAEADVAVYVCOQYYS 118

QY 121 PLTFGAGTKLELKRVTAAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNAL 180
DB 119 PPTFGGKTKVEIKRTVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNAL 178

QY 181 QSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 240
DB 179 QSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 238

RESULT 4
US-11-158-505-3
; Sequence 3, Application US/11158505
; Publication No. US2006002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 3
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody light chain construct
; US-11-158-505-3

Query Match      83.7%; Score 1040; DB 7; Length 238;
Best Local Similarity 84.6%; Pred. No. 1.8e-61;
Matches 203; Conservative 15; Mismatches 20; Indels 2; Gaps 1;

QY 1 MDSQAQVLMLLLVWSGTGDI VMSQSPDSLAVSLGERVTLNCKSSQSLYSGNQKNYLA 60
DB 1 METDTILLWLLWVPGSTGDI VMTQSPDSLAVSLGERATINCASQSDYDGD--SYMN 58

QY 61 WYQKPGQSPKLLIYWASARESGVPRFSGSGGTDFLTITSSVQAEADVAVYVCOQYYS 120
DB 59 WYQKPGQSPKLLIYWASARESGVPRFSGSGGTDFLTITSSVQAEADVAVYVCOQYYS 118

QY 121 PLTFGAGTKLELKRVTAAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNAL 180
DB 119 PPTFGGKTKVEIKRTVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNAL 178

QY 181 QSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 240
DB 179 QSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 238

RESULT 5
US-11-158-505-25
; Sequence 25, Application US/11158505
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QY	1	MDSQAQVLMLLLLWVSGTCGDIWVMSQPSDSLAVSLGERVTLNCKSSQSLLYSGNOKNYLA	60
DB	1	METDTTLLWLLWVPGSGTDIVMTQSPDSLAVSLGERATINCKASQSDVDYDGD--SYMN	58
QY	61	WYQKPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFTLTISSVQAEADVAVYVCOQYYSY	120
DB	59	WYQKPGQSPKLLIYVASNLESGVDPDRFSGSGSGTDFTLTISSLQAEADVAVYVCOQSLQD	118
QY	121	PLTFGAGTKLELKRITVAAPSVFIPPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL	180
DB	119	PPTFGGKTKEIKRITVAALS VFIPPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL	178
QY	181	QSGNSQESVTEQDSKDSYLSLSTLTLSKADYEHKHYVACEVTHQGGLSSPVTKSFNRGEC	240
DB	179	QSGNSQESVTEQDSKDSYLSLSTLTLSKADYEHKHYVACEVTHQGGLSSPVTKSFNRGEC	238
RESULT 10			
US-11-158-505-19			
; Sequence 19, Application US/11158505			
; Publication No. US20060002921A1			
; GENERAL INFORMATION:			
; APPLICANT: WINSOR-HINES, DAWN			
; APPLICANT: RAO, PATRICIA			
; APPLICANT: RINGLER, DOUGLAS J			
; APPLICANT: PONATH, PAUL			
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE			
; TITLE OF INVENTION: INDUCTION IN PRIMATES			
; FILE REFERENCE: TILN-031			
; CURRENT APPLICATION NUMBER: US/11/158,505			
; CURRENT FILING DATE: 2005-06-21			
; PRIOR APPLICATION NUMBER: 60/582,181			
; PRIOR FILING DATE: 2004-06-22			
; NUMBER OF SEQ ID NOS: 76			
; SOFTWARE: Patentin Ver. 3.3			
; SEQ ID NO 19			
; LENGTH: 238			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1			
; OTHER INFORMATION: antibody light chain construct			
US-11-158-505-19			
Query Match 82.9%; Score 1030; DB 7; Length 238;			
Best Local Similarity 84.2%; Pred. No. 7.9e-61;			
Matches 202; Conservative 15; Mismatches 21; Indels 2; Gaps 1			
QY	1	MDSQAQVLMLLLLWVSGTCGDIWVMSQPSDSLAVSLGERVTLNCKSSQSLLYSGNOKNYLA	60
DB	1	METDTTLLWLLWVPGSGTDIVMTQSPDSLAVSLGERATINCKASQSDVDYDGD--SYMN	58
QY	61	WYQKPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFTLTISSVQAEADVAVYVCOQYYSY	120
DB	59	WYQKPGQSPKLLIYVASNLESGVDPDRFSGSGSGTDFTLTISSLQAEADVAVYVCOQSLQD	118
QY	121	PLTFGAGTKLELKRITVAAPSVFIPPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL	180
DB	119	PPTFGGKTKEIKRITVAALS VFIPPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL	178
QY	181	QSGNSQESVTEQDSKDSYLSLSTLTLSKADYEHKHYVACEVTHQGGLSSPVTKSFNRGEC	240
DB	179	QSGNSQESVTEQDSKDSYLSLSTLTLSKADYEHKHYVACEVTHQGGLSSPVTKSFNRGEC	238
RESULT 11			
US-11-158-505-74			
; Sequence 74, Application US/11158505			
; Publication No. US20060002921A1			
; GENERAL INFORMATION:			
; APPLICANT: WINSOR-HINES, DAWN			
; APPLICANT: RAO, PATRICIA			



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; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-28

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Qy      121 PL-TFGAGTLELKGRTVAAPSVFIFPPSDEQLKSGTASVVCCLNFFYPREAKVOMKVDNA 179
Db      116 PMCSFGOGTKLEIKRIVAAPSVFIFPPSDEQLKSGTASVVCCLNFFYPREAKVOMKVDNA 175
Qy      180 LOSGNSQESVTEODSKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPTKSFNRGE 239
Db      176 LOSGNSQESVTEODSKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPTKSFNRGE 235
Qy      240 C 240
Db      236 C 236

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